The Complexity of Family Life Courses in 20th Century Europe and the United States

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CHAPTER 1

INTRODUCTION

Scholars and the general public alike perceive modern life courses to be more complex, unstable, and unpredictable than in the early and mid-20th century (Walsh 2012; Beck 1994; 2009; Sennet 2006). Common narratives in family sociology and demography surrounding more complex family trajectories revolve around the decline of the modern nuclear family and the pluralization of family forms (Bengtson 2001). Indeed, both the United States and several European countries experienced a decrease and postponement in marriage and marital fertility that coincided with an increase in nonmarital cohabitation and fertility as well as divorce and remarriage (Cherlin 2010; Buchmann & Kriesi 2011; Sobotka & Toulemon 2008). This increase in the number of family events and states that individuals experience over the course of their lives resulted in more complex family trajectories (Brückner & Mayer 2005). In family demography, this dramatic shift in behavior is conceptualized as the Second Demographic Transition (SDT) (Van de Kaa 1987; Lesthaeghe 1995; 2010; 2014). However, the onset and speed of the SDT varies greatly across countries (Sobotka 2008). The trend towards less marriage and parenthood is more pronounced in northwestern Europe and the United States than in southern and eastern Europe.

Increasing family life course complexity may have serious consequences for individuals and societies. Complexity generated by early nonmarital parenthood, serial cohabitation, and divorce is likely tightly intertwined with the production of social inequalities and their reproduction across generations (e.g., McLanahan & Percheski 2008). Social policies that address single precarious events, such as divorce, will be less able to maintain the economic and subjective wellbeing of individuals with complex trajectories where disadvantageous events accumulate across the life course (e.g., Dannefer 2003). Further, increasingly complex lives may be associated with population decline, which has been framed as a problem for social welfare systems in many European countries. As family life courses become increasingly unpredictable, men and women may delay parenthood considerably and remain childless involuntarily (Schmidt et al. 2012). This might not only affect individuals' wellbeing in later adulthood, but may contribute to the decline of fertility rates and population size.

Family sociologists and demographers have a long history of developing, utilizing, and updating heuristics to understand patterns of family formation. The first of these, the family life cycle, was developed by Paul Glick (1947; 1989) as a framework to study mid-20th century American family lives. The family life cycle assumes that most Americans progress from being single, entering marriage, followed by parenthood, then experiencing an empty nest, and finally death or widowhood. While the framework of a universal family life cycle was an accurate description of American experiences from the 1940s to the 1960s (Cherlin 2010), it proved to be too static for the complex family lives following the onset of the SDT. Moreover, it was of limited use for many European countries with a relatively high prevalence of childlessness and stepfamilies on account of First and Second World War casualties (e.g., Wagner 1997). In its stead, a differential life course framework emerged that identified and accounted for variations in family lives across birth cohorts and countries (Mayer & Müller 1986; Mayer & Schoepflin 1989). The life course framework is widely accepted among family scholars and has led to a multitude of studies on how socio-historic context and individual agency interact to structure life course patterns (Mayer 2009; 2004).

Despite the theoretical, conceptual, and methodological developments surrounding the SDT and the life course framework, our understanding of family life course complexity is incomplete. For example, although Elzinga & Liefbroer (2007) demonstrate how family life course complexity varies across countries and birth cohorts, no studies have described how complexity varies within societies, e.g. across educational groups. Further, no research has attempted to explain why the complexity of family trajectories varies across and within countries and cohorts. The overarching aim of this dissertation is to begin to fill this gap. First, I address three descriptive research questions in the second chapter: 1) how does family life course complexity vary across birth cohorts, 2) how does it vary across countries, and 3) does it vary more across birth cohorts or across countries (see chapter 2).[1] Second, I take a macro-level approach on whether and how family policies are associated with complexity (see chapter 3), followed by a micro-level approach on whether parental resources are associated with complexity and whether this association has changed across birth cohorts (see chapter 4). Fourth, going beyond traditional micro- and macro-sociological approaches, I estimate the extent that complexity is attributable to genetic factors using a biodemographic approach (see

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chapter 5). Finally, I close with a discussion of my contributions, the limitations of my conceptualization and operationalization of life course complexity, and an outline of an integrated framework for future research (see chapter 6).

The following sections of this chapter introduce important concepts and theories pertaining to family life course complexity. First, I briefly discuss how life course terminology and concepts have been incorporated in research on the transition to adulthood. Second, relevant family demographic trends in the United States and Europe are briefly reviewed. Third, based on those insights, I conceptualize family life course complexity in terms of life course transitions and unpredictability. The conceptualization and operationalization of complexity is discussed more thoroughly in chapter 2. Third, I apply traditional sociological and demographic perspectives on family demographic behavior as well as a socio-genomics approach to theorize life course complexity. Finally, I conclude the introduction by situating the following chapters within the theoretical background.

The Transition to Adulthood and Family Formation

Family life course research is often situated within the empirical and theoretical literature on the transition to adulthood (Furstenberg 2010; 2008; Billari & Liefbroer 2010; Billari & Wilson 2001). The transition to adulthood is a demographically dense phase between age 18-35, during which US and European young adults leave the parental home and establish independent households, form cohabiting and marital relationships, and enter parenthood (Cook & Furstenberg 2002). The theoretical and empirical literature on the transition to adulthood has been heavily influenced by life course theory, incorporating numerous life course concepts and principles (Hogan & Astone 1986).

The transition to adulthood and family formation consists of a series of life course states. Life course states are defined by social statuses or social roles, often related to age (Settersten & Mayer 1997). The prevalence or occurrence of a life course state reflects how common a given state is within a population, usually a birth cohort within a country. Life course transitions denote a move from one life course state to another (George 1993). Two life course states are said to be tightly coupled or highly synchronized if transitions between the two states are common within a population. Sequencing indicates the order in which life course states and transitions occur (Hogan 1978). Life course scholars are often interested in the duration individuals spend in a life course state before transitioning to another (Elder et al. 2003, p.10).

A life course trajectory or pathway is a sequence of life course transitions between life course states of a given duration (Wheaton & Gotlib 1997).

The transition to adulthood is an institutionalized pathway, indicating that the occurrence of states, the transitions between them as well as their ordering are regulated by formal and informal norms and rules (Mayer & Müller 1986; Mayer & Schoepflin 1989). For example, members of society hold attitudes towards the ideal age to transition to a certain life course state, which may or may not be socially sanctioned if violated (Liefbroer & Billari 2010). State regulations on the age of marriage directly institutionalize life courses. In mid-20th century Europe and the United States, a successful transition to adulthood encompassed completing compulsory education, leaving the parental home, entering the labor market, forming a marital union, and finally entering parenthood, more or less in that order (Buchmann 1989). To disentangle the role of family processes in the social stratification of pathways to adulthood, I concentrate on those states and transitions directly pertaining to family formation: leaving the parental home, forming (and dissolving) unions, and entering parenthood.

Family Demographic Trends in 20th Century United States & Europe

In the following discussion, I briefly sketch trends in the occurrence of life course states and transitions related to leaving the parental home, forming and dissolving unions, and entering parenthood. Where appropriate, I mention trends in the synchronicity of transitions or their de-coupling. Trends in the sequencing of family life courses are summarized near the end of this section. Periodically, I discuss differences by gender, which are commonly similar across countries and birth cohorts. More specific information on how these trends vary by gender, race, and socioeconomic status can be found in the following chapters.

The transition to adulthood and family formation often begins with leaving the parental home. The age at which individuals transition out of the parental household declined in the early and mid-20th century, but has recently began to increase in the United States and many European countries (Goldscheider 1997; White 1994; Vogel 2002). For example, the percentage of US women age 18-24 living in the parental home increased from 34.9 % in 1960 to 49.2 % by 2010.[2] A similar trend can be observed for men, although men tend to live in the parent home longer than women. However, there are considerable cross-national differences: individuals

[2] U.S. Census Bureau, Current Population Survey, March and Annual Social and Economic Supplements. U. S. Bureau of the Census, 1980 Census of Population, PC80-2-4B, "Persons by Family Characteristics," table 4. 1970 Census of Population, PC(2)-4B, table 2. 1960 Census of Population, PC(2)-4B, table 2.

leave home earliest in northwestern European countries and the United States, followed by eastern and southern European countries (Mulder et al. 2002; Billari & Wilson 2001; Billari 2004). Between 1991 and 2004, 15 % of Danish men lived in the parental home between age 20-23, while 56 % of German men and 89 % of Italian men still lived in the parental home (Iacovou 2010). It has also become more common to return to the parental home, especially for young adults experiencing economic hardship (Mitchell 2006; Stone et al. 2014). In the United States, 36 % of young adults born between 1980-1984 returned to the parental home at least once by age 27 (Sandberg-Thoma et al. 2015).

Destinations after leaving the parental home have become more diverse. For the first half of the 20th century, leaving the parental home and entering marriage were tightly coupled life course transitions (Buchmann & Kriesi 2011). In fact, only 5 % of unmarried US men and women lived outside the parental home in the early 20th century (Rosenfeld 2007). However, there are again substantial cross-national differences: although living independently before entering marriage is a more recent development in the United States, it was fairly common in Sweden. For example, nearly 50 % of Swedish women born between 1930-1939 lived outside the parental home before entering marriage (Billari & Liefbroer 2010). For more recent birth cohorts, individuals regularly form independent households or live in cohabiting unions after leaving the parental home rather than marrying (Evans 2013; Zorlu & Mulder 2011).

Although the median age of first marriage has increased across all European countries and the United States, the median age of first union has remained constant, with the exception of southern Europe (Manning et al. 2014; Buchmann & Kriesi 2011). The stability in the age at first union is largely attributable to higher rates of cohabitation offsetting lower rates of marriage (Perelli-Harris & Lyons-Amos 2015; Kiernan 2001; Smock 2000; Goldstein & Kenney 2001). The percent of the US population living in non-marital cohabitation increased from 0.6 % in 1960 to 6 % in 2010, while the percentage living in a marital union decreased from 69 % to 54 % for men and 65 % to 52 % for women.[2] Cross-national differences in the age at first union as well as cohabitation rates are large. Generally, cohabitation rates are higher and the transition to marriage is later and less common in Scandinavian countries compared to western European countries and the United States, followed by southern and eastern European countries (Sobotka & Toulemon 2008). In the United States, the median age of first marriage in 1960 was 22 for men and 20 for women, which increased to age 28 for men and 26 for women by 2010.[3] In Poland, where marriage is still widely prevalent, the median age of marriage has

[3] U.S. Census Bureau, Current Population Survey, March and Annual Social and Economic Supplements

only increased moderately from age 22 to 23 for women born in the 1930s compared to the 1970s (Billari & Liefbroer 2010). During the same time window, the median age of marriage increased from 23 to 31 for Swedish women.

One reason for the decrease in marriage, especially in the United States, is the increase in divorce. Between 1960 and 1980 , the crude divorce rate in the United States more than doubled from 2.2 to 5.2 (Amato 2010). It has since decreased to 3.6 divorces per 1,000 marriages by 2006. While marital unions in northwestern and southern Europe are less likely to end in divorce, some eastern and central European countries have divorce rates that are similar to the United States. The crude divorce rate in 2007 was 3.0 in the Czech Republic and 2.8 in Belgium and Germany, but only 2.0 in the Netherlands and 0.8 in Italy (Amato & James 2010). The US doesn't just exhibit higher rates of marital dissolution than many European countries, but cohabiting unions in the US are shorter and more likely to end in separation (Smock 2000). The median duration of Swedish cohabiting unions is 3.4 years with 46 % ending in marriage, compared to 4.2 years and 46 % in France, and 1.7 years and 75 % in Switzerland (Heuveline & Timberlake 2004). Schnor (2014) demonstrates that compared to West Germany, cohabiting unions with children are more stable in East Germany, where cohabitation is more prevalent and accepted. However, cohabitation is not just a life course state for young adults. Higher rates of marital separation have not only increased remarriage rates, but also rates of cohabitation later in adulthood as an alternative to remarriage (Coleman et al. 2000; Xu et al. 2011).

The decline of fertility across Europe and the United States to near- or sub-replacement rates has concerned both scholars and policymakers (Balbo et al. 2013). Low total fertility rates may result from delayed entry into parenthood, the tempo effect, as well as smaller family sizes and higher rates of childlessness, the quantum effect (Morgan & Taylor 2006). As was the case with other family demographic trends, fertility trends differ starkly across countries. Between cohorts born during the 1930s and the 1970s, the median age of women's first birth has remained low and stabile near age 23 in eastern Europe, but has risen from age 24 to 29 in Scandinavian countries and from 26 to 29 in southern and western Europe (Billari & Liefbroer 2010). In the United States, women's median age at first birth rose from age 23 to 25 between the 1940s and 1980s birth cohorts (Finer & Philbin 2014). Cohort fertility for women born in 1940 compared to 1965 dropped from 2.2 to 1.9 children per woman in Denmark, compared to 2.1 to 1.6 in Austria, 2.0 to 1.7 in Greece, and 2.0 to 1.8 in the Czech Republic (Billari 2005). Completed fertility is comparatively high in the United States: between 2.0 to 2.2 for women born in the 1960s (Zeman et al. 2018). After remaining low for mid-20th century birth cohorts, childlessness among the 1970s female birth cohort reached levels previously held by cohorts born during the 1920s: approximately 15 % in Sweden, France and the United States, and over 20 % in Germany and Italy (Sobotka 2017; Frejka 2017). In sum, the decrease in period total fertility rates across the late 20th century is likely more associated with fertility delay rather than fertility decline (e.g., Morgan & Taylor 2016).

Men and women transitioned into parenthood directly after their transition into marriage for most of the 20th century in all European countries and the United States (Corijn & Klijzing 2001; Kiernan 2001; Sobotka & Toulemon 2008). However, the two life course states have become increasingly independent from one another. The percentage of women entering parenthood before marriage increased dramatically in practically all northwestern European countries between the 1930s and 1970s birth cohorts: from 20 % to 58 % in Sweden, from 5 % to 51 % in France, and from 6 % to 56 % in Ireland (Billari & Liefbroer 2010). However, the majority of nonmarital births, especially in Scandinavian countries, occur within cohabiting unions rather than to single mothers (Thomson 2014). In fact, the percentage of births to lone mothers has remained relatively constant across birth cohorts in Europe. The United States represents an exception: the percentage of nonmarital births among women under age 44 increased from 21 % in the early 1980s to 28 % in the early 1990s (Bumpass & Lu 2000). However, only 29 % and 39 % of these nonmarital births occurred to cohabiting couples.

The decoupling of parental home leaving with marriage and of marriage with parenthood has made research on the sequencing of early life course events more important. While some scholars use multistate event history analysis or life table modeling to study variation in life course origins and destinations (e.g., Schoen et al. 2007; Zeng et al. 2012; Billari 2001), sequence analysis has emerged as a popular method to describe and visualize holistic life course trajectories (Abbott & Tsay 2000; MacIndoe & Abbott 2004; Aisenbrey & Fasang 2010). There are commonly three steps in sequence analysis: First, each trajectory is operationalized as a sequence by aligning an individual's life course states in chronological order with their respective durations. Second, the dissimilarity of each sequence pair is estimated using distance measures that indicate the degree of difference between any two sequences. Finally, a clustering algorithm is applied to group sequences into distinct units that are maximally homogenous. Sequence analysis reduces the complexity of life course data in two ways: First, sequence analysis identifies common life course pathways within multitudes of trajectories that may warrant further study. Second, rather than analyzing numerous "point in time outcomes", such as the age of first birth, sequence analysis enables researchers to analyze life courses that amount from those outcomes, a single "process outcome" (Abbott 2005).

A number studies have used sequence analysis to identify life course patterns and how they vary across countries and birth cohorts (Baizan et al. 2002; Bras et al. 2010; Hofäcker & Chaloupková 2014; Robette 2010; Raab et al. 2014; Aisenbrey & Fasang 2017; see also Van Winkle 2018 as chapter 2). Billari and Liefbroer (2010) concisely summarize the change in the transition to adulthood across birth cohorts in their study countries as a shift from an early, contracted and simple pattern to a late, protracted and complex pattern. However, comparative studies on the trend towards a more complex transition to adulthood have observed persistent cross-national differences (Mills & Blossfeld 2005; Corijn & Klijzing 2001; Fokkema & Liefbroer 2008; Sobotka & Toulemon 2008). Early home leaving into singlehood, followed by the early formation of cohabiting unions, and late parenthood and marriage is relatively common in Scandinavian countries, while late parental home leaving into marriage and parenthood is more common in southern Europe. Young adults in central and eastern Europe as well as the United States tend to leave home somewhat later than in Scandinavian countries, but early marriage and parenthood is more common.

Conceptualizing Family Life Course Complexity

The life course states within each of the dimensions discussed above – residence, unions, and parenthood – are often studied as independent spheres of the family life course (for example, see the reviews by Cherlin 2010; and Buchmann & Kriesi 2011). When two dimensions are studied simultaneously, it is generally union formation and parenthood (e.g., Thornton & Philipov 2009; Kiernan 2001; Hiekel & Castro-Martín 2014; Baizán et al. 2004). However, it is important to consider the intersections of these dimensions as separate and qualitatively different life course states. For example, the social meaning and consequences of entering nonmarital parenthood within the parental home differs starkly from entering nonmarital parenthood outside the parental home (Kaphingst et al. 2014). Naturally, this approach to identifying life course states increases the number of distinct states, some of which may be empirically scarce, e.g. divorced with children in the parental home.

There is general agreement that complexity should be conceptualized in terms of life course differentiation (Mayer 1991; Mayer et al. 2010; Elzinga & Liefbroer 2007; Biemann et al. 2011; Van Winkle & Fasang 2017). Brückner and Mayer (2005) define differentiation as an increase in the number of life course states experienced across the life course. Therefore, complexity has often been operationalized using a simple count measure of the number of life course states or transitions experienced across individuals' lives. However, complexity is also associated with an increase in life course uncertainty (Beck 1994; 2009; Sennett 1998; 2006). Composite metrics developed in sequences analysis have been developed that incorporate both the number of life course states as well as the degree of unpredictability (Elzinga & Liefbroer 2007; Gabadinho & Studer 2010; see Van Winkle 2018 as chapter 2 for a mathematical definition and further discussion). Sequence based complexity measures have the advantage that they can incorporate a large number life course states, i.e. the intersection of different life course dimensions, as well as a small number of simple states.

However, there is little research on the complexity of family trajectories using sequence based complexity metrics. The bulk of studies that do incorporate these nuanced indicators are interested in the differentiation of education-work-retirement trajectories (Biemann et al. 2011; Ciganda 2015; Riekhoff 2016; 2018; Van Winkle & Fasang 2017). Although there are many studies that apply sequence and cluster analysis to family trajectories, only Elzing and Liefbroer (2007) study the complexity of early family life courses in a number of countries and birth cohorts. They find that average early family life course complexity had only increased moderately across a small number of their study countries Otherwise, average complexity had remained relatively stable. Further, they found that average complexity tends to be lower in eastern and southern Europe compared to northwestern Europe. Their study, although exceptional, concentrated on the development of sequence based metrics and remained descriptive. Further, they only studied life courses up to age 35, likely missing events later in life, such as divorce and remarriage. There is a clear need for more cross-national and cross-temporal research on the complexity of family life courses that span the entire reproductive life course. This is the remit of chapter 2. It is also important to gain an understanding of the possible determinants of complexity by first assessing the associations between individual and societal characteristics, and the complexity of family trajectories, which is the remit of chapters 3-5.

Theoretical Background

Three meta-theoretical narratives have been applied when studying single family life course events and transitions: one cultural, one economic, and one institutional (see White 1994 for parental home leaving; Smock 2000 for cohabitation; Amato & James 2010 for divorce; Balbo et al. 2013; and Morgan & Taylor 2006 for fertility). First, the SDT thesis is an ideational account, which attributes changes in family demographic behavior across birth cohorts to a cultural shift from materialism to post-materialism (Van de Kaa 1987; 2001; Lesthaeghe 1995; 2010; 2014). According to the second account, increasing economic uncertainty in lieu of globalization and deindustrialization has induced the decline of marriage and parenthood across advanced economies (Mills & Blossfeld 2003; 2005; 2013). This perspective incorporates arguments on socioeconomic resources and the timing of marriage and parenthood (Oppenheimer 1988; 1994; Easterlin 1975; 1976). Proponents of the third account, mostly life courses sociologists and welfare state scholars, regularly argue that labor market and family policies influence family decisions and generate cross-national differences in family life courses (Esping-Andersen 1990; 1999; Mayer 1997; 2004; 2009). Policies influence rational decision-making processes by altering the costs and benefits of family demographic behavior (Becker 1974; 1981). There is however a fourth, still emerging, theoretical perspective: biodemography (Kohler et al. 2006; Mills & Tropf 2015; Conley 2016). This approach highlights the interplay between genetic factors behind family demographic behavior and external societal characteristics. In the following discussion, I review these theories related to the complexity of holistic family life courses rather than single life course events.

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The SDT thesis is likely the most prominent cultural account of changing family demographic behavior. At the core of the SDT thesis lies the assumption that individuals' value orientations and normative beliefs are the predominant determinates of their decisions regarding union formation and parenthood (Lesthaeghe 2010). The decline of standard and simple patterns of marriage and parenthood and the increase in complex family patterns result from an ideational shift from materialist to postmaterialist values (Lesthaeghe 1995; Lesthaeghe & Johan Surkyn 1988). The SDT as a theory, rather than a descriptive concept (e.g. Mclanahan 2004), has a relatively long history and has been continually revised in the face of empirical challenges and theoretical criticism (Lesthaeghe 2014; see Zaidi & Morgan 2017 for a review).

The SDT was originally formulated by van de Kaa (1987; see also Lesthaeghe & Van de Kaa 1986) to describe the decline of fertility to sub-replacement levels in many European countries between 1955 and 1970. Van de Kaa (1987) argues that the temporal link between marriage and parenthood weakened as the war generation in Europe married early to initiate sexual relations during the Second World War, but waited to enter parenthood until after the war ended. The link between sexual relations and marriage weakened further for the postwar generation as divorce rates increased, which in turn lead to less marriage and more cohabitation. Finally, it became socially acceptable to enter parenthood outside of marriage. For van de Kaa and Lesthaeghe (1986), the shift from parents with a “king child” to a child with “king parents” (see Aries 1980) is a central cultural component of this process. Aries (1980) argues that the motivation for childbearing, and also small family sizes, had shifted. While the war generation reduced family sizes for economic security and upward mobility, the postwar generation entered parenthood only if a child was central to their self-actualization.

Since its formulation, the SDT theory has been continually revised, especially by Lesthaeghe (1995; 2010). In its current form, the SDT theory posits a universal and irreversible increase in the mean age at marriage and parenthood, a lower propensity to marry and enter parenthood, as well as a higher prevalence of cohabitation, divorce and non-marital childbirth (Zaidi & Morgan 2017). The current argument is more focused on the relationship between childhood circumstances, the development of value orientations, and consequent family behavior. The postwar generation grew up in a time of unprecedented economic growth and stability. For these cohorts, basic and intermediary needs in the Maslowian hierarchy, e.g. safety and security, were always met, which induced a drift towards the highest-order needs of self-actualization and individual autonomy (Maslow 1943). Highly educated individuals from higher socioeconomic backgrounds are expected to be the forerunners of this value shift and therefore forerunners of the SDT (Lesthaeghe & Johan Surkyn 1988). It is assumed that the high and long-term commitments of marriage and parenthood are incompatible with the pursuit of self-fulfillment and individualistic life styles. In sum, a shift towards postmaterialism, especially among highly educated individuals, lead to more complex family life courses.

The SDT theory has been challenged on both empirical and theoretical fronts (see Lesthaeghe 2010 for a summary and a response). Many current trends in family demographic behavior discussed above correspond with the SDT, especially higher rates of cohabitation and the postponement of marriage and parenthood (Ortega 2014; Cherlin 2012; Zeman et al. 2018). However, a number of trends are not consistent with the SDT. For example, although marriage rates decreased and divorce rates increased in the last half of the 20th century, many countries have seen these rates plateau or even reverse (Ohlsson-Wijk 2011; Schoen & Standish 2001). Further, fertility rates have increased slightly and may reach replacement levels in some Nordic countries (Andersson et al. 2009). Contrary to a convergence of family life course patterns across countries, empirical evidence demonstrates persistently divergent patterns of family demographic behavior (Fokkema & Liefbroer 2008; Billari & Wilson 2001). Finally, results on the association between postmaterialism and behavior associated with the SDT are mixed

(Gubernskaya 2010; Bystrov 2014; Surkyn & Lesthaeghe 2004 with positive associations; Lesthaeghe & Lopez-Gay 2013; Van de Kaa 2001 with no or negative associations).

Recently, the SDT theory has come under increasing pressure to incorporate gender systems into its framework (Berrnhardt 2004). Van de Kaa (1987) refers to gender-egalitarian norms within the context of increasing postmaterialism, but was less attentive to the gender specific meanings and consequences of individualization for family related decisions (Solsona 1998). McDonald (2000) and Goldscheider (2000) argue that below-replacement fertility, the decline in marriage, and the increase in divorce and cohabitation may be the result of higher gender equity in the public sphere compared to the private sphere. Confronted with the reversal of fertility rates in some Scandinavian countries, Lestheage (2010) contends that gender values related with the SDT, i.e. gender egalitarianism, may lead to a recuperation of completed fertility. However, Esping-Andersen & Billari (2015) and Goldscheider & colleagues (2015) have formulated formal gender equity theories that stand in contrast with the SDT theory. Esping-Andersen & Billari (2015) maintain that the shift to below-replacement fertility is the fourth phase in standard demographic transition theory (see Kirk 1996 for a summary of demographic transition theory), which is caused by a lag between gender equity in the public and private spheres. Once this lag is overcome, societies will transition to a fifth stage characterized by fertility recuperation. Goldscheider & colleagues (2015) extend their argument to union stability. Rather than a lag between gender equity in the public and private spheres, they argue more specifically that fertility will increase and divorce will decrease when men's roles have adapted to women's modern roles.

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Perhaps the largest competitor of the SDT thesis has become Mills & Blossfeld's (2003; 2005; 2013) argument that globalization and increasing economic uncertainty is an integral factor behind change in family life courses. Globalization, although an unwieldy concept, can be understood as the process by which national economies become increasingly interdependent by means of an accelerated international trade of goods, services, and capital (Brinkman & Brinkman 2002). Globalization is usually associated with more competitive global markets, economic tertiarization, technological advancements, and new human resource strategies, which together diminish manufacturing jobs in the primary sector and polarize the occupational structure (Kalleberg 2012; 2009; 2000). The general argument is that young adults facing economic uncertainty in a globalized world economy delay marriage and parenthood due to the high costs of long commitments, and resort to other family models instead, e.g. cohabitation.

Links between economic uncertainty and delayed or foregone family formation can be traced back to the sociological literature of the 1970s and 1980s. For example, Oppenheimer (1988) argues that young adults spend time on the marriage market to find an "acceptable" match. Individuals use information currently available to estimate the future characteristics of a potential partner. For example, women use men's current labor market status to estimate their future socioeconomic attainment. However, as unstable, temporary, and low-wage employment as well as unemployment became more common, men need more time to establish themselves on the labor market (Oppenheimer & Kalmijn 1995). Hence, delayed marriage is the consequence of increasing uncertainty on the marriage market. Oppenheimer (1988) additionally suggests that increases in childless cohabitation may reflect a cost effective strategy to prolong the search for an acceptable partner. According to Easterlin (1975; 1976), delayed entry into parenthood is the result of a conflict between consumption aspirations and children. Young adults are expected to enter parenthood once they have achieved their desired standard of living that was formed during childhood. Poor labor market conditions make it more difficult for young adults to fulfill their consumption aspirations, which leads to postponed or foregone parenthood.

In sum, globalization is linked with postponed or forgone marriage and parenthood as well as increased rates of cohabitation, divorce and non-marital births (Mills & Blossfeld 2003; 2005; 2013). More simply, rising economic insecurity is associated with more complex family life courses. However, globalization does not affect all members of society equally, but has differential impacts depending on individuals' position in the social structure. Increased economic uncertainty during young adulthood may increase the importance of parental resources for family formation, because children rely more on their parents for economic support (Furstenberg 2008). Parents are motivated to invest in their children to minimize the risk of downward social mobility (Breen & Goldthorpe 1997). Moreover, socioeconomically advantaged parents further compensate for their children's lacking resources to ensure their socioeconomic success (Bernardi & Grätz 2015; Erola & Kilpi-Jakonen 2017). Parental background may influence children's family life courses indirectly through educational attainment or labor market attainment (Erola et al. 2016). However, parents may also find ways to directly affect their children's family lives, for example by supporting independent living as an alternative to marriage.

Young adults from higher socioeconomic backgrounds are more likely to attend and graduate higher education institutions (e.g. Steelman & Powell 1991). There are three reasons why students in higher education delay marriage and parenthood (Mills & Blossfeld 2005): First, young adults in higher education are in an economically precarious situation for a longer period of time. Second, students that additionally work during their studies have less leisure time, which may decrease their willingness to make family commitments (Mills 2000). Finally, prolonged education requires that young adults maintain their role as a student longer before transitioning into roles associated with work and family. Following tertiary education, parents with high education and incomes may facilitate a smooth labor market entry and provide financial support for marriage and parenthood, e.g. weddings and childcare. Indeed, some studies have demonstrated that fertility and marriage rates as well as union stability have become highest among the highly educated (Andersson et al. 2009; Ohlsson-Wijk 2011; Lyngstad 2004). In sum, the family life courses of young adults from advantaged backgrounds are increasingly less complex than those from disadvantaged backgrounds as economic uncertainty continues to increase.

Parental resources beside income and education may also be increasingly important for young adults' family demographic behavior. McLanahan's (2004) diverging destinies hypothesis contends that the association between childhood family structure and children's socio-economic and family outcomes has become stronger over time. Specifically, the outcomes of children from single parent households are increasingly less favorable compared to those from two parent households. Indeed, children from single parent families in the United States are younger when they leave the parental home (Goldscheider & Goldscheider 1998), form a cohabiting union (Teachman 2003), and enter parenthood (Hofferth & Goldscheider 2010). These patterns have also been observed in European countries, such as Germany (Raab 2017; Bernhardt et al. 2005).

Aside from economic hardship, i.e. parental income and education, three mechanisms may account for the association between children's family structure and their family demographic behavior: socialization, social control, and stress (see Teachman 2003 for an overview). First, parents may explicitly or implicitly transfer their values and preferences regarding family formation. Indeed, numerous studies have found evidence of the intergenerational transmission of fertility (Fasang 2015), cohabitation (Teachman 2003), marriage and divorce (Amato & DeBoer 2001; Wolfinger 2011) as well as holistic family trajectories (Fasang & Raab 2014). Second, two-parent families may be able to control and supervise the activities of their children more effectively than single-parent families (Astone & McLanahan 1991; Thomson et al. 1992). For example, single parents may have greater difficulty in regulating behavior that reduces the risk of teenage pregnancy for their children, such as contraceptive use (Miller 2002). Finally, family instability, generated through divorce and re-partnering, is related with higher stress levels and behavioral problems during childhood (Fomby & Cherlin 2007) and with early union formation and parenthood (Fomby & Bosick 2013). Therefore, childhood family structure may be increasingly associated with the complexity of family trajectories.

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The economic uncertainty perspective concentrates on cross-temporal variation. However, it also suggests that national institutions filter the negative effects of globalization, thereby generating cross-national differences in family life course complexity. Comparative life course sociologists have long analyzed how variations in national labor market and family policies structure work and family lives (Mayer & Müller 1986; Mayer & Schoepflin 1989). Early comparative literature relating family polices to life course outcomes drew comparisons between broad welfare state regimes. Esping-Andersen's (1990; 1999) well-known typology differentiates countries into social democratic, conservative, and liberal welfare state regimes based on labor market and social institutions. Ferrera (1996) later extended this typology to include a southern European regime type (see chapter 2 for a discussion of the relationship between welfare state types and the complexity of family trajectories). Family policy scholars adapted these typologies to categorize countries based on cash support for families and support for working parents (e.g., Lewis 1992; Gornick et al. 1997). While social democratic countries, such as Sweden, are characterized by universal state support for working families, liberal countries, such as Ireland, are characterized by low and targeted state support for families. Both conservative and southern European countries are characterized by less public support for families and working parents, however cash transfers tend to be more generous in conservative countries (Gauthier 2002).

More recent literature has shifted from broad welfare state regime types to identifying specific policy dimensions. Family policy dimensions are groups of policies and legislation that have similar goals. For example, Thévenon (2011) identifies six dimensions of modern family policy: 1) the reduction of poverty and income maintenance, 2) direct compensation for the economic cost of children, 3) fostering (women's) employment, 4) improving gender equity, 5) support for early child development, and 6) raising birth rates. Policy dimensions have at least two advantages over regime classifications: First, they allow a more nuanced understanding of how family policy differs between countries as well as within countries across time (Baldwin 1996).

Second, broad welfare state typologies can be of limited use for studies on concrete outcomes, because they are concerned with many areas of social policy and life course outcomes.

There are three policy dimensions that can be identified in the comparative welfare state regime and family policy literature: familization, defamilization, and liberalization. First, familizing policies aim to support the traditional family characterized by relational obligations between husband and wife as well as between parents and children (Mätzke & Ostner 2010; Saraceno 2016). Specifically, familizing policies incentivize and enable a male-breadwinner female-homemaker division of labor. A common example of familizing policies are child allowances, which compensate for the economic costs of children, but also increase the inhibition threshold of women's employment (Esping-Andersen 1999; Leitner 2003).

Defamilizing policies are often identified as the opposite of familizing policies. Originally, the concept of defamilization was developed as a critique of Esping-Andersen's (1990) typology, which was based on a gender-neutral concept of decommodification, i.e. individual protection from market forces through state institutions (Lister 1994). Until recently, defamilization has been used to indicate policies that enable women to commodify themselves, i.e. participate in the labor market and establish independent households (Esping-Andersen 1999). More recent literature has broken with the conceptualization of a familization-defamilization continuum. Following Daly (2011), Lohmann and Zagel (2016) argue that defamilization should be conceptualized as individualization, because defamilizing policies foster individualism by reducing gender and intergenerational dependencies through state support to individuals. Common examples of defamilizing policies are universal child and elder care as well as job-protected and well-paid parental leave. These policies not only enable women to more easily balance work, family, and care responsibilities, but also facilitate a gender egalitarian division of labor.

Liberalizing family polices are often overlooked in the traditional welfare state literature (e.g. Ermisch 1986). Liberalizing policies aim to reduce restrictions, increase individual autonomy and freedom, and shift gendered power relationships surrounding family demographic decisions (e.g. Hobson 1990). These policies differ from defamilizing policies, because they directly affect family demographic processes and events, e.g. childbirth and union formation. Prime examples of liberalizing policies instituted across many European countries during the 1960s and 1970s are abortion by request and no-fault divorce legislation. Abortion by request legislation gives women more autonomy over the decision whether and when to enter parenthood (Levine et al. 1999). Similarly, no-fault divorce legislation enables individuals, especially women, to more easily end a martial union (Gruber 2004; González & Viitanen 2009). Other, more recent, examples of liberalizing policies are universal access to assisted reproduction technologies and the legal treatment of informal relationships, i.e. cohabitation.

Common theoretical approaches on how family policies affect family life courses assume that family demographic events, such as parenthood and divorce, are rational decisions (Becker 1974; 1981; Becker et al. 1977; Becker & Tomes 1994; see Gauthier 2007 for a discussion). According to rational choice approaches, such as Becker's (1981) New Home Economics, a family demographic decision is a utility maximization process. This process is conceived as a function of the (opportunity) costs and benefits of a family demographic event that are additionally subject to economic constraints and preferences. Therefore, family policies influence individuals' family demographic decisions by increasing or reducing the (opportunity) costs or benefits of family demographic events. Note that costs and benefits can be both economic, such as (forgone) income, or social, such as stigmata. Other, more sociological, theoretical approaches on the influence of family policy on family life courses stress that policies are a reflection of culture and what society deems as "normal" forms of private life (Strohmeier 2002). Family policies then act to construct opportunities or restrictions on biographical options.

Familizing policies incentivize early marriage and parenthood within marriage as well as a male-breadwinner female-homemaker division of labor (Leitner 2003; Gauthier 2007). Direct transfers, e.g. family or child allowances, reduce the economic costs of entering parenthood, but are often conditional on women caring for children. Indirect transfers, e.g. tax benefits for married couples, generally increase the benefits of marriage and also reduce the costs of parenthood. Saraceno (2016) brands these transfers as supported familism, because they enable individuals within families to uphold traditional care responsibilities regardless of economic constraints. In contrast, unpaid and unprotected parental leave schemes are implicitly familizing, not least because they increase both the social and economic costs of leave schemes being used by fathers rather than mothers (Lohmann & Zagel 2016).

Defamilizing policies reduce the benefits of marriage and parenthood within marriage, because traditional care obligations are less institutionalized around marriage (Kröger 2011; Lister 1994). These policies commonly outsource care responsibilities to the public sphere, which may facilitate a gender egalitarian division of labor within partnerships (Lohmann & Zagel 2016; Saraceno 2016; Esping-Andersen 1999). For example, public childcare and eldercare that is widely available, of high quality, and affordable reduces care obligations within families. Short-term, well-paid, and job-protected parental leave systems aimed at both mothers and fathers facilitate women's quick return to the labor market after childbirth and a more active childrearing role for fathers. In turn, cohabitation, non-marital parenthood, and divorce become more attractive compared to early marriage and parenthood.

Similarly, liberalizing family policies reduce the attractiveness of early marriage and parenthood by enabling alternative options. Becker, Landes, and Michael (1977) argue that liberal divorce legislation reduces the value of marriage, which may lead to less marriage and more non-marital births. However, others have argued that liberal divorce legislation reduces the commitment and therefore the costs of marriage, which may lead to more marriage, divorce, and remarriage (Alesina & Giuliano 2006). Liberal abortion legislation has been shown to lower fertility rates, but may also reduce early marriage and parenthood (Levine et al. 1999). In sum, familizing policies reduce the complexity of family life courses, because these policies actively or implicitly incentivize early marriage and parenthood. Defamilizing and liberalizing policies increase the complexity of family trajectories, because these policies decrease the costs of alternatives to early marriage and parenthood.

Timing is a central to how and to what extent experiences and institutions affect individuals' life courses (Elder et al. 2003). The experiences of individuals during early life have path dependent and often cumulative effects on later life outcomes (Dannefer 2003). The idea that early interventions influence outcomes later in life is widespread in the social policy literature, especially in the social investment literature (e.g., Kuitto 2016; Nolan 2013; Hemerijck 2015). For example, investment in early childcare and education is argued to have higher returns for society than investments in adult education, i.e. higher taxable incomes and lower poverty risks.

The experience of family policies during early adulthood will likely have a greater influence on the complexity of family life courses than experiences during prime or mature adulthood. For example, the extent of familizing policies, e.g. family allowances and unpaid parental leave, that individuals experience during their early 20s will likely have large and path dependent effects. Men and women will be more likely to enter marriage and parenthood early if familizing policies are in place while they are young, which may reduce the number of transitions and stages later in life. Similarly, defamilizing and liberalizing policies that reduce the attractiveness of early marriage and parenthood will likely have large and long-lasting effects if they are already implemented early in the life course. However, familizing and defamilizing policies may influence couples' decisions for higher parity births after entering marriage and parenthood. Further, liberal divorce legislation will enable marital separation at any age.

Nonetheless, policies that are first implemented when individuals have already married and entered parenthood may be less likely to influence the complexity of their family life courses.

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While the meta-theoretical perspectives discussed above are the most prominent in family demography and sociology, biodemographic research has gained importance in the last decades (see D'Onofrio & Lahey 2010 for a review; see Conley & Fletcher 2017 for an introduction to socio-genomic research). Biodemography is the study of family demographic behavior that incorporates both economic and sociological theories with approaches from biology, especially behavioral and molecular genetics (Kohler et al. 2006). Discounting biological and genetic accounts may lead to grossly biased results, especially if genetic factors are confounded with associations between social factors and life course complexity (D'Onofrio & Lahey 2010). Therefore, sociologists and demographers interested in family life course complexity need to add the biodemographic approach to their theoretical and methodological repertoire.

The estimation of heritability is the first step to incorporate biodemography into the study of complexity. Heritability is a population level characteristic and reflects the genetic component of a trait or phenotype, here complexity. Specifically, heritability is the proportion of phenotypic variance that is attributed to genetic variance, i.e. to common genetic variants within a population, as opposed to environmental variance (Domingue et al. 2016b; see chapter 5 for a mathematical definition). The strength of heritability gives researchers insight on the potential importance of sociobiological explanations and the consequence of ignoring them. Note the important difference between the sociological concept of intergenerational transmission and the biodemographic concept of heritability. Intergenerational transmission denotes the similarity between parents and their children regardless whether this similarity arose through genetic or environmental factors, or a mixture of the two. Heritability in contrast is similarity between two individuals, related or not, attributable only to genetic factors.

Sociological research has a long, sometimes dubious, tradition of estimating the heritability of social outcomes (e.g. Galton 1869).[4] For much of the 20th century, twin studies were the gold standard for estimating the genetic component of a given trait (Neale & Cardon 1992; Boomsma et al. 2002). A common analytical approach, the ACE model, compares monozygotic and

[4] For example, Frances Galton was also the first to coin the term eugenics and provided a theoretical foundation for Social Darwinism during the 19th century (Gillham 2001).

dizygotic twins to decompose variance into an additive genetic component (A)[5], a component attributable to common environmental factors, e.g. family background (C), and an environmental component unique to each twin (E) (see Diewald et al. 2015 for a brief discussion). Although sociologists have been mainly interested in quantifying the effects of family background (C), twin studies also demonstrate that many components of family life course complexity are heritable (A). The heritability of women's age at first birth has been estimated to be between 0 in Denmark to 0.3 in the UK. This means that genetic influences account for up to 30 % of the total variation of Danish women's age at first birth, but none in the UK. The heritability of completed fertility has been estimated to be between 0.24 for Swedish and 0.43 for Danish women, and between 0.24 for Swedish and 0.28 for Danish men (Kohler et al. 1999; Tropf et al. 2015; Mills & Tropf 2015). Johnson and colleagues (2004) estimate large heritabilities in the propensity to marriage in the US: 0.72 for women and 0.66 for men. Estimates for the propensity to divorce are similarly high, between 0.52 and 0.59 for both US men and women (McGue & Lykken 1992; Jocklin et al. 1996).

However, twin ACE models come with strong assumptions, which lead to biased heritability estimates if violated (Horwitz et al. 2003). For example, it is assumed that monozygotic and dizygotic twins are treated identically and that dizygotic twins share an average of 50 percent of their genes (Conley et al. 2013). Further, heritability estimates from twin studies may not be generalizable if there is non-random genetic stratification, e.g. genes associated with high fertility are more common among twins (Mills & Tropf 2015). Recent advances in molecular genetics and low-cost DNA sequencing methods has enabled researchers to base heritability estimates on true genetic similarity rather than assumed genetic similarity (Domingue et al. 2016). Molecular geneticists, as opposed to quantitative behavioral geneticists, are primarily interested in isolating and locating genetic variants associated with a trait, rather than estimating the heritability of a trait (Conley 2016). Genome wide associational studies (GWAS) are commonly used to locate single nucleotide polymorphisms (SNPs), markers of genetic variation, that are associated with a trait. Complex traits, such as fertility or cognitive ability, are polygenic traits that are affected by multiple SNPs, rather than a single gene. Following GWAS, polygenic risk scores (PGS) that estimate individuals' genetic predisposition for a certain trait are constructed. The variance that PGSs explain are often only a fraction of

[5] Examples of non-additive genetic effects are epistasis, i.e. interactions between genic variants, dominance deviations, suppression of genetic variants through other genetic variants, and gene-environment interactions.

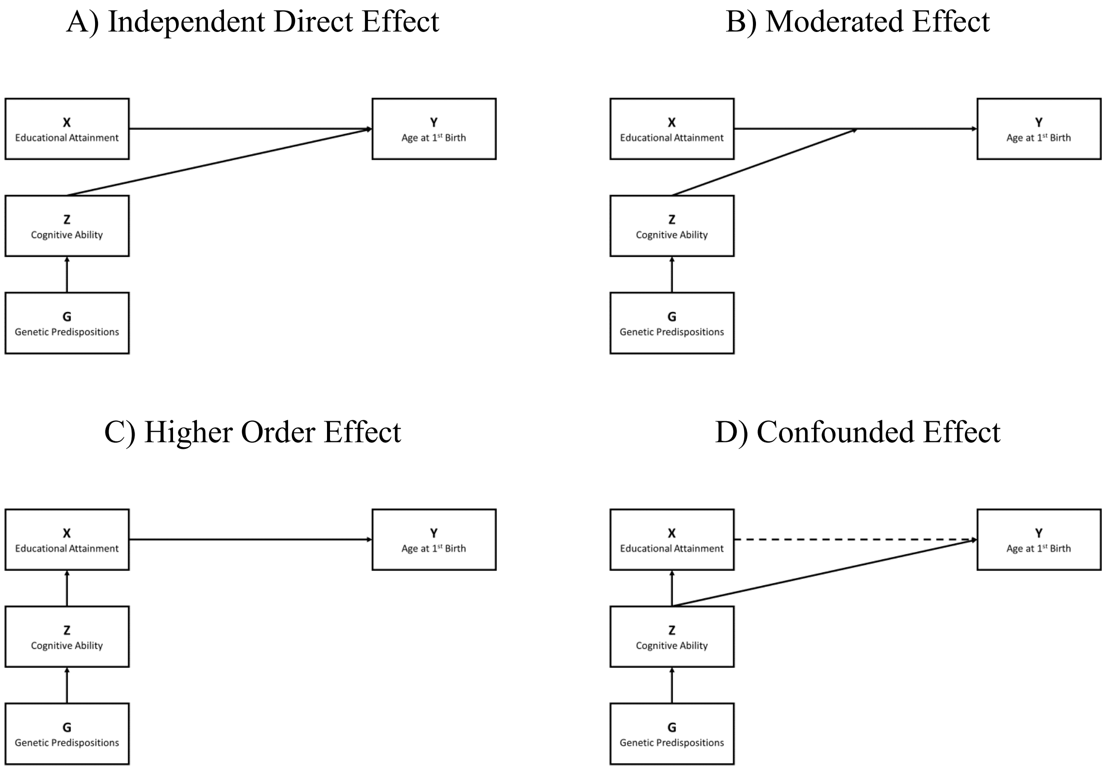
heritability estimates from twin models (see Zuk et al. 2012; Eichler et al. 2010 for a discussion on the problem of missing heritability).

Genome-wide complex trait analysis (GCTA) consists of several analytical approaches to estimate heritability based on all available SNPs. The most common method is a genomic-relatedness-based restricted maximum-likelihood (GREML) model, which utilizes genetic similarity to decompose the total variance of a trait into a genetic and an environmental component (Yang et al. 2011; 2010). GREML studies have been used to estimate the heritability of several anthropomorphic and some social demographic outcomes (Domingue et al. 2016b). Tropf and colleagues (2015b) recently estimated a 0.08 SNP heritability for completed fertility and a 0.15 SNP heritability for the age of first birth for a pooled sample of women from the UK and the Netherlands. SNP heritability estimates from GREML are generally larger than PGS heritability estimates, but still lower than twin based heritability estimates. A study by Yang and colleagues (2015) demonstrates that SNP heritability of height from GREML using the entire genome with imputed SNPs rather than a sample of SNPs are similar to those from twin studies. Tropf and colleagues (2016) establish that low GREML estimates for fertility may result from pooling samples across countries and cohorts, which masks important gene-environment interactions. There are currently no studies that estimate SNP heritabilities for family demographic outcomes aside from fertility, such as marriage or divorce. However, based on the large heritabilities found in twin studies, it is likely that both life course states are highly heritable.

Exactly how genetic factors influence social demographic traits remains largely unclear (see Udry 1996 for an overview of early biosocial models for fertility). Kohler and colleagues (2006) argue that genetic predispositions affect fertility 1) directly through biological pathways, e.g. menarche, 2) indirectly through conscious life course decision-making, e.g. knowledge about fecundity, and 3) indirectly through subconscious life course decision-making, e.g. personality characteristics. Freese (2008) contends that any genetic effect is mediated through the body, which he terms the “phenotypic bottleneck”. He discusses four pathways how genes influence outcomes through intermediate phenotypes and how sociological explanations may be affected.

The biosocial pathways identified by Freese (2008) are displayed in Figure 2 with a stylized example. In the upper-left panel of Figure 1, genetic factors, G, partially determine the intermediate phenotype cognitive ability, Z, which affects the timing of first birth, Y (see Davies et al. 2016; Kirkpatrick et al. 2014 for the heritability of cognitive ability; see Haaga 2001 for the association between cognitive ability and fertility). Educational attainment, X, has an independent direct effect on the age at 1st birth in panel A. In panel B, cognitive ability moderates the association between educational attainment and fertility, while in panel C cognitive ability simply precedes educational attainment. Finally, panel D demonstrates how cognitive ability is confounded with education. This is an especially worrisome case for sociological research, because estimated effects between two social phenomena, e.g. education and fertility, will often be biased if genetic factors remain unobserved.

Figure 1: Ideal Type Pathways for Genetic Effects on Sociological Relationships through Intermediate Phenotypes



Note: Figure adapted from Freese (2008)

GCTA-GREML approaches have been used to estimate heritabilities for several sociological outcomes and anthropomorphic traits (see Domingue et al. 2016b for a broader overview). Height is estimated to be between 35 % and 56 % heritable, while BMI estimates are slightly lower, between 0.27 and 0.43 (Conley et al. 2014; Yang et al. 2015). Davies and colleagues (2016) estimate heritabilities of 31 % for verbal-numeric reasoning, 5 % for memory, and Kirkpatrick and colleagues (2014) estimate that general cognitive ability is 35 % heritable. Heritability estimates for educational attainment lie between 0.17 and 0.33 (Boardman et al.

2015; Conley et al. 2014), while social deprivation and household income is an estimated 21 % and 11 % heritable, respectively (Hill et al. 2016). Even socioeconomic status during childhood and across the life course has been estimated to be between 18 % and 19 % heritable (Marioni et al. 2014; Trzaskowski et al. 2014). Considering the consistent findings for the relevance of genetic influences, it seems plausible that family life course complexity will also be affected by genetic factors both directly, e.g. biologically determined fecundity, and indirectly, e.g. phenotypes that affect family demographic decisions.

The relevance of genetic factors for family life course complexity may vary across social contexts, e.g. across birth cohorts. Societal norms and institutions can change the heritability of social outcomes by influencing the relationship between intermediate phenotypes and outcomes. As an example outside of family demography, Domingue and colleagues (2016a) find evidence that the heritability of smoking in the United States increased from roughly 0.13 to 0.32 between cohorts born 1939-1945 and 1947-1959. They conclude that as evidence on the dangers of smoking emerged during the 1960s, the influence of genetic factors associated with nicotine addiction strengthened. Using historical twin data, Bras and colleagues (2013) report evidence for increasing heritability during the first demographic transition in 19th century. They argue that genetic predispositions for fertility became more important as social control of women's fertility decreased. In these examples, environmental changes, i.e. knowledge on the effects of smoking and decreased social control, increased the effect of genetic factors, which in turn increased the heritability.

In family demography, the most common hypothesis is that the heritability of family demographic outcomes will be higher for cohorts transitioning to adulthood after the onset of the SDT. Udry (1996) proposes a multilevel biosocial model, where societal characteristics influence the relationships between genetic predispositions and outcomes. Specifically, the genetic influence on voluntary behavioral outcomes, e.g. entering parenthood and marriage, will decrease in societies with a high level of social constraints. Udry (1996, p.335) argues that in egalitarian and individualistic contexts, behavioral variation will increase and genetic predispositions will have more opportunities to express themselves. Indeed, studies using twin data observe higher heritabilities for Danish cohorts transitioning to adulthood after the onset of the SDT for fertility (Kohler et al. 1999; 2002; Rodgers et al. 2001). Tropf and colleagues (2015a) also find that the heritability of UK women's age at first birth increased for cohorts characterized by liberalization and the sexual revolution, but that the introduction of modern contraception and economic recessions decreased heritabilities shortly after. It seems likely that the heritability of family life course complexity will increase for birth cohorts who transitioned to adulthood in societies characterized by the SDT.

Structure of the Dissertation

The remainder of my dissertation is structured around the four meta-theoretical perspectives on family life course complexity discussed above. The following, second chapter introduces the concept of family life course complexity and its operationalization using the sequence complexity index in detail. The following three empirical chapters therefore refrain from a detailed discussion of sequence complexity in their respective methods sections. The second chapter specifically enquires how family life course complexity varied across European countries during the 20th century and how complexity varied across birth cohorts in Europe. This chapter puts change over time in perspective with cross-national differences. This innovative methodological approach, simultaneously decomposing complexity into portions attributable to country and cohort specific differences using cross-classified random effect modeling, calls the SDT account into question. Although I do find an increase in family life course complexity across Europe, these differences are almost negligible compared to considerable variation across countries. I conclude the second chapter with a discussion on how incorporating concepts of social change by means of cohort replacement as well as social policy could increase the empirical validity and prediction power of the SDT thesis.

The following three chapters are empirical chapters, which test hypotheses that were foreshadowed in the discussion above. Each of these short empirical chapters include only a small introduction rather than a lengthy theoretical review, followed by a section outlining the data and methods, a summary of the results, and a brief discussion. The first of these empirical chapters, my third chapter, focuses on the association between family policy and family life course complexity. In this chapter, I test whether and how familizing, defamilizing, and liberalizing family policies are associated with complexity. Further, I analyze whether the timing of family policy in the life course, e.g. whether policies were implemented while an individual was younger or older, matters. To do this I generate policy indices using a wide range of indicators from 15 European countries between 1924-2008, such as the availability of child or family allowances, the length of paid parental leave, and the legalization of divorce and abortion. Indeed, I find associations that are consistent with the comparative welfare state and differential life course literature. However, my findings have implications for how family policy should be measured and included in life course analyses.

My fourth chapter takes a micro-perspective and assesses the relationship between socioeconomic background and family life course complexity in light of globalization and increasing economic insecurity. Specifically, I analyze whether the association between parental resources and early family life course complexity has grown stronger across birth cohorts. This chapter concentrates on cohorts born in the United States between 1961-1964 and 1980-1984. I focus on the United States, because of its lack of social and labor market institutions that mitigate the negative effects of globalization in many European welfare states. Therefore, the family is the last resort for young adults seeking support during their transition to adulthood and family formation. My results support the economic insecurity framework, but also McLanahan's (2004) diverging destinies framework.

My fifth and last empirical chapter incorporates a biodemographic approach to the study of family life course complexity. I use GCTA-GREML on a sample from the US Health and Retirement Study to estimate the SNP heritability of family life course complexity and its components across birth cohorts. This is not only the first socio-genomic study of holistic life courses, but also the first heritability estimates for union formation and dissolution using a molecular genetics approach. While I do show moderate heritability for family life course complexity, I do not find strong evidence for increasing heritability across cohorts. I conclude that scholars interested in variation in heritability across socio-historic contexts should not just concentrate on the level of social constraints within a society, but also on the universality of those constraints.

In my final chapter, I conclude with a review of my contributions to the theoretical literature on the complexity of family trajectories, followed by a discussion on the limitations of my conceptualization and operationalization of complexity. It is especially important to differentiate between quantitative increases in family life course complexity and the different qualitative meanings that individuals attach with complexity. I also discuss whether increasing family life course complexity should be considered a worrisome development or interpreted in a more optimistic light. Finally, I introduce an integrated framework to guide future research on family life course complexity in Europe and the United States as well as in other global contexts.

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CHAPTER 2

Family Trajectories Across Time and Space: Increasing Complexity in Family Life Courses in Europe?

Family life courses are thought to have become more complex in Europe. This study uses SHARELIFE data from 14 European countries to analyze the family life courses of individuals born in 1924–1956 from ages 15 to 50. A new methodological approach, combining complexity metrics developed in sequence analysis with cross-classified multilevel modeling, is used to simultaneously quantify the proportions of variance attributable to birth cohort and country differences. This approach allows the direct comparison of changing levels of family trajectory differentiation across birth cohorts with cross-national variation, which provides a benchmark against which temporal change may be evaluated. The results demonstrate that family trajectories have indeed become more differentiated but that change over time is minor compared with substantial cross-national variation. Further, cross-national differences in family trajectory differentiation correspond with differences in dominant family life course patterns. With regard to debates surrounding the second demographic transition thesis and the comparative life course literature, the results indicate that the degree of change over time tends to be overstated relative to large cross-national differences.

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Introduction

Many scholars have claimed that patterns of family formation and living arrangements have undergone great changes in European societies during the twentieth century (for a review, see Buchmann & Kriesi 2011). Young adults leave the parental home, marry, and enter parenthood at later ages (A. Gauthier 2007; Settersten 2007), and the odds of returning to the parental home as well as never entering marriage or parenthood have increased (Goldscheider 1997; Rowland 2007). Additionally, cohabitation (e.g., Heuveline & Timberlake 2004), divorce (e.g., Schoen & Canudas-Romo 2006), remarriage (e.g., Coleman et al. 2000), and single parenthood (e.g., Heuveline et al. 2003) have become more common. Billari and Liefbroer (2010) spoke of a shift from an early, contracted, and simple to a late, protracted, and complex transition to adulthood. Thomson (2014) emphasized that more complex families are produced through lone childbirth, union dissolution, repartnering and stepfamily childbearing well after the transition to adulthood is complete.

A shift toward more complex family life courses is consistent with the concept of the second demographic transition (SDT). Family demographers have used the SDT (Lesthaeghe & Van de Kaa 1986; Van de Kaa 1987) to account for changes in family behavior through a universal value shift toward postmaterialism within and across societies. However, recent research has displayed stable or growing cross-national differences rather than convergence as suggested by the SDT thesis (Billari & Wilson 2001; Mills & Blossfeld 2005; Corijn & Klijzing 2001; Elzinga & Liefbroer 2007; Fokkema & Liefbroer 2008; Sobotka & Toulemon 2008). Life course sociologists have emphasized institutional variations to account for these cross-national differences, arguing that welfare states shape individual family life courses both directly (Mayer & Müller 1986; Mayer & Schoepflin 1989) and indirectly (Mayer 2004). Although these two perspectives may not be mutually exclusive accounts of family life course variation, they do emphasize very different dimensions of variation: change across time versus differences across countries.

The aim of this study is not only to investigate (1) how family life courses vary across historical time (i.e., birth cohorts), and (2) how family life courses vary across countries, but especially (3) whether family life courses vary more across birth cohorts or across countries.

Despite the wide discussion around cross-temporal and cross-national variation in family formation, the comparative literature has compared family trajectories either across birth cohorts within a single country (Baizan et al. 2002; Bras et al. 2010; Chaloupková 2010; Robette 2010) or between a small set of countries (Potarca et al. 2013; see Elzinga & Liefbroer

2007 for a notable exception). However, no research has attempted to directly compare change in family formation over historical time with cross-national differences (for notable exceptions in other fields, see Fowler et al. 2016 on ethnoracial diversity; Günther & Harttgen 2016 on realized fertility intentions; Van Winkle & Fasang 2017 on employment trajectories). Research that puts change over time in direct perspective with differences between countries is important because it can provide a benchmark against which change over time can be evaluated. Further, research that directly compares temporal and cross-national variation simultaneously informs two of the most prominent research traditions in comparative family demography and sociology: the ideational account of the SDT and the institutional arguments of comparative life course sociology.

I contribute to the comparative literature by introducing a new methodological approach that enables researchers to directly compare change across birth cohorts with cross-national differences in longitudinal life courses. Specifically, I simultaneously quantify family life course variation across birth cohorts and variation across countries by incorporating a sequence based metric in cross-classified multilevel regressions. This methodological approach enables me to put changing levels of family trajectory complexity across birth cohorts in perspective with cross-national variation. Further, I demonstrate how other researchers can expand on this methodological approach by estimating conditional cross-classified models. This allows me to investigate relationships between individual characteristics and family formation complexity as well as the extent to which individual characteristics account for variation across birth cohorts and countries.

I use sequence analysis to conceptualize family formation holistically, as a long life "process outcome" (Abbott 2005). Abbott conceptualized process outcomes as global results of multiple individual events (such as job spells within careers) as opposed to point-in-time outcomes, which are the results of a process (such as pension amounts). Although many have used sequence analysis to study family processes (e.g., Elzinga & Liefbroer 2007; Fasang & Raab 2014; Raab et al. 2014), the majority of the literature concentrates on events in the early life course as a part of the transition to adulthood. However, changes in family life courses need to be studied as a lifelong process because changes associated with the SDT affect the timing of multiple life course events, their sequencing, and the occurrence of new events in later life, such as divorce and remarriage. Using retrospective data from the Survey of Health, Ageing and Retirement in Europe (Börsch-Supan et al. 2013; Schröder 2011), I am able to observe family formation until age 50 for men and women born from 1924 to 1956 in 14 European countries.

Theoretical Background

Conceptualizing Complexity in Family Trajectories

How should increasing complexity in family life courses be conceptualized? Concepts surrounding increasing family life course complexity are used ambiguously in the literature (see Brückner & Mayer 2005). *Differentiation* (Mayer 1991) generally refers to variation within individual life courses, and *institutionalization* (Kohli 1997; Mayer & Müller 1986) and *standardization* (Modell & Furstenberg 1976) refer to variation between life courses. Other concepts such as individualization (Beck & Beck-Gernsheim 1994) and pluralization (Brüderl 2004) have been used less systematically. It is essential to develop clearly defined concepts prior to their operationalization to ensure valid measurement of family trajectory complexity.

I conceptualize increasing complexity in family formation as differentiation. Brückner and Mayer (2005) developed a comprehensive categorization of life course variation that occurs either within individual life courses over the lifetime or between individual life courses within a population. They defined differentiation as a process whereby life courses are characterized by an increasing number of distinct life course states. Differentiation further implies increasing unpredictability and uncertainty in individual life courses. Examples of family formation differentiation are when unmarried cohabitation precedes marriage or a first union is followed by divorce and further unions. Contrary to differentiation, *de-differentiation* refers to a process whereby the number of distinct life course stages decreases. Family life courses become de-differentiated if high-parity families are replaced by single-child families.

Family Trajectories Across Time

The SDT thesis is the most prominent account of family life course differentiation. Van de Kaa (1987, p.11) postulated the establishment of a new demographic regime following four shifts: from marriage to cohabitation, from child-centric to pair-centric relationships, from precautionary contraception to conception for self-fulfillment, and from uniform to pluralistic families. The change in demographic behavior associated with the SDT, such as cohabitation and childlessness, is accounted for by a shift from materialism to postmaterialism (van de Kaa 2001). The higher-educated and socioeconomically advantaged act as forerunners of this value shift toward self-actualization and nonconformism as well as the forerunners of more complex family demographic behavior associated with it (Lesthaeghe 1995; Lesthaeghe & Johan Surkyn 1988; Sobotka 2008).

Cohorts born in the mid- to late 1920s just entered courtship age as World War II began. Those cohorts that experienced World War II or its aftermath in Europe held primarily materialist values associated with securing economic and social standing. The family formation patterns of these early industrialist and industrialist cohorts are considered to have been relatively simple, consisting mostly of leaving the parental home early and entering directly into marriage, followed by parenthood (Mayer 2004). Cohorts born in the early and mid-1950s entered courtship age during the 1970s. Stable economic growth and the expansion of welfare state and educational systems facilitated a value shift toward postmaterialism among the early members of this postindustrialist and contraceptive revolution cohort. According to the SDT thesis, this shift toward self-actualization led to postponed marriage and parenthood as well as an increase in cohabitation, childlessness, and divorce. Therefore, I expect that *family trajectories have become more differentiated across birth cohorts* (Hypothesis 1 (H1)).

Family Trajectories Across Countries

Proponents of the SDT have used institutional arguments to account for cross-national variation in family demographic behavior. For example, Lesthaeghe (2010, pp.244–245) argued that the foundations of traditional family formation patterns will weaken first in egalitarian liberal market democracies that respect individual choice despite normative ideals. Comparative life course sociologists focus on institutions and their impact on family formation (see Mayer 2009). At the core lies the proposition that welfare regimes, labor market institutions, and educational systems shape societal life course patterns. Institutions may influence life courses directly by means of age gradation (Mayer & Schoepflin 1989) or indirectly by incentivizing the adherence to dominant life course patterns or enabling individuals to tread new paths (Breen & Buchmann 2002; Buchmann 1989).

Esping-Andersen's (1990) "worlds of welfare capitalism" typology has been widely used as a heuristic to classify and compare European countries (see Arts & Gelissen 2002; Emmenegger et al. 2015). The extended typology developed by Esping-Andersen (1999) clusters countries based on levels of decommodification (i.e., protection from labor market risks) and defamilization (i.e., public assumption of family care tasks). Although the *social democratic regime* is characterized by universal and generous social protection as well as public child and elderly care, the *liberal regime* provides only limited welfare benefits, and childcare is privately arranged. Unfortunately, common representatives of the liberal welfare state regime type (e.g., the UK and Ireland) did not participate in the survey used in this study (SHARELIFE), or the data was not available when the analyses were performed. Social protection is targeted toward specific groups and is less generous in the *conservative regime* and in the *Mediterranean regime*, but families are especially responsible to compensate residual welfare coverage in the latter. Eastern European countries were considered to constitute an authoritarian welfare state during state socialism. Following their transition to liberal market democracy, scholars have debated whether these countries still compromise a single welfare regime or have shifted to existing models (Aidukaite 2009).

Scandinavian social democratic welfare states were forerunners in the implementation of defamilizing and individualizing family policies, which reduced gender and intergenerational dependencies and allowed greater freedom in family formation (Lohmann & Zagel 2016). In Sweden, paid and job-protected maternity leave was introduced in 1955 and was supplemented by paternal leave in 1974 (DICE 2015).[6] In Denmark, publicly funded childcare for children within one year after birth was introduced as early as 1964 (Garrouste 2010). Further, generous old-age benefits following retirement and unconditional old-age pensions were introduced in Sweden in 1953 and 1913, respectively.[7] These policies allowed cohorts born in the early 1930s to maintain a high labor market attachment after entry into parenthood and when elderly family members were in need of care. High female labor force participation rates coupled with high levels of decommodification safeguard individuals, especially women, from economic downturns (DiPrete et al. 1997) as well as life course risks, such as divorce and single parenthood (DiPrete 2002). Therefore, the social democratic welfare regime reduces the costs and risks of family demographic behavior associated with more complex family life courses, such as cohabitation, nonmarital childbirth, and divorce.

Contrary to welfare systems in Scandinavian countries, the social protection systems and family policies in conservative continental European countries incentivize a male breadwinner–female homemaker division of labor. Many western and central European countries implemented family and child allowances before maternity leave and well before any paternal leave policies (Gauthier & Monna 2004; DICE 2015). For example, Austria introduced family allowances in 1967, paid and job-protected maternity leave in 1974, and paternal leave in 1990. Further, publicly funded childcare in most continental countries is available only for children starting at

[6] Maternity leave is defined as a minimum of 14 weeks paid and job-protected leave of absence according to the International Labour Organization (ILO) convention on maternity leave. Paternal leave is defined as a minimum of one week paid and job-protected leave of absence following childbirth or maternity leave for fathers as part of a parental leave scheme.

[7] See ILO Ratifications of Social Security Convention, 1952 (No. 102) (http://www.ilo.org/dyn/normlex/en/f?p=NORMLEXPUB:11300:0::NO::P11300_INSTRUMENT_ID:312247) and the Country Fact Files of HelpAge International (http://www.pension-watch.net/country-fact-file/).

age 3 (Garrouste 2010). The concentration of family policy on family allowances and maternity leave rather than childcare and paternal leave incentivizes traditional family formation by making women primary care providers and limiting female labor market participation (Gottschall & Bird 2003; Morel 2007). Gendered decommodification and highly familistic policies make family behavior associated with complex family formation, such as divorce and single parenthood, highly costly, especially for women.

In southern Europe, authoritarian regimes (e.g., Mussolini in Italy and Franco in Spain) coupled with the moral teachings of the Greek Orthodox and Roman Catholic churches contributed to the production of a welfare model with the family at its center (Flaquer 2000). For example, maternity leave was introduced in 1976 in Spain and 1984 in Greece (DICE 2015). Without widespread early childcare and paternal leave policies, childcare has to be arranged by the family, usually by women. A late introduction of unconditional old-age benefits additionally burdened families when elderly family members need care. These welfare states are additionally characterized by highly gendered labor market segmentation and very low rates of female labor market participation as well as a context in which families must compensate for low levels of benefits following unemployment or income loss (M. Ferrera 1996). Consequently, processes that produce family complexity are very risky in the context of Mediterranean welfare states, and reliance on families to secure individual welfare often leads to a dramatic delay in leaving the parental home.

Generally, levels of decommodification and defamilization were high in eastern European countries, comparable with social democratic countries, during the era of state socialism. For example, East Germany introduced maternity leave in 1950, early childcare in 1965, and paternal leave in 1972 (Garrouste 2010; Maul et al. 2009). However, many societies encouraged early marriage and implemented pronatalist policies (Fodor et al. 2002; Kreyenfeld 2004), thereby incentivizing traditional family formation processes. Although the family trajectories of very young cohorts may be differentiated to a greater extent following the turbulent transition to liberal market democracy, this is not likely the case for cohorts born before the 1970s.

In sum, defamilizing and decommodifying institutions characteristic of social democratic welfare states reduce the risks of complex family formation patterns involving cohabitation, single parenthood, and divorce. Gendered decommodification in conservative welfare states enables men to peruse more complex family patterns similar to social democratic welfare states but incentivizes less complex patterns of early marriage and parenthood for women. Familism in southern Europe and natalism during state socialism in eastern Europe promotes less-complex family patterns consisting of early marriage and parenthood. Therefore, I expect that *family trajectories are most differentiated in social democratic countries (Sweden and Denmark), followed by conservative countries (Austria, West Germany, the Netherlands, France, Switzerland, and Belgium), and least differentiated in southern European countries (Spain, Italy, and Greece) as well as in eastern European countries (the Czech Republic, Poland, and East Germany)* (Hypothesis 2 (H2)).

Comparing Family Trajectories Across Time and Space

Across all countries, family formation differentiation resulting from a shift toward postmaterialism can be conceived as the result of cohort replacement (Ryder 1965). Inglehart (1990) predicted levels of postmaterialism to increase as young cohorts raised in socioeconomically secure contexts gradually replace older cohorts. Similarly, levels of differentiation within countries will gradually rise as younger cohorts with more-complex family trajectories replace older cohorts with relatively simple trajectories. In a world devoid of institutional arrangements that influence family formation differently across countries, levels of family formation differentiation could be expected to increase at similar rates across countries.

However, changes in institutional arrangements that influence family formation have lagged the shift toward postmaterialism in most European countries. Studies have demonstrated that for cohorts born as early as 1946, postmaterialists became increasingly common across continental European countries (Abramson & Inglehart 1986; Inglehart 2008). In certain countries, such as West Germany and the Netherlands, postmaterialism had become predominant among the entire population by the late 1970s and early 1980s. Nevertheless, paternal leave was not implemented until 1986 in West Germany and 2009 in the Netherlands, and neither country has yet to introduce universal early childcare. Although social democratic institutions in Scandinavian countries enabled postmaterialists to follow alternative family pathways, institutions in continental Europe inhibited complex family formation even as postmaterialism became ever more common. Therefore, I expect that *family trajectory variation across birth cohorts is country-specific* (Hypothesis 3 (H3)), rather than a contemporaneous process across countries.

Social change through cohort replacement is generally a slow process but will be especially slow when institutions impede behavior that would correspond with ideational change.

Pronounced increases in family formation differentiation require not only postmaterialist socialization at a relatively early age but also institutional arrangements that correspond to new family formation patterns involving cohabitation, single parenthood, and divorce. In light of the large cross-national differences in family trajectories (Billari 2004; Billari & Wilson 2001; Blossfeld et al. 2005; Corijn & Klijzing 2001; Elzinga & Liefbroer 2007; Sobotka & Toulemon 2008), it is unlikely that variation across birth cohorts will be larger than variation across countries before defamilizing institutions are integrated across European welfare states. I therefore expect that *family trajectory differentiation varies more across countries than across birth cohorts* (Hypothesis 4 (H4)).

Data and Methods

Study Sample and Sequence Definition

I use the third wave of SHARE,[8] SHARELIFE, which consists of retrospectively collected life history data on multiple life domains—such as partnership, family demographics, living arrangements, and employment—for a number of birth cohorts and countries (Börsch-Supan et al. 2013; Schröder 2011). The SHARELIFE population consists of individuals born before 1957 and their partners, and the data set contains information on 26,768 individuals born between 1908 and 1984. Family life course trajectories are operationalized as sequences using the SHARELIFE accommodation, retrospective children, and partner modules. My sample consists of individuals born between 1924 and 1956 in 14 European countries. I exclude individuals born before 1924 because of insufficient sample sizes. All individuals born after 1956 are partners of SHARELIFE respondents that must be excluded from the analysis. Their inclusion leads to grossly underestimated complexity values for cohorts born after 1956 because individuals who never married, or divorced and never repartnered, would not be included in the sample.

[8] This article uses data from SHARE Waves 1, 2, and 3 (SHARELIFE) (Borsch-Supan 2017a, b, c). See Börsch-Supan et al. (2013) for methodological details. The SHARE data collection has been primarily funded by the European Commission through FP5 (QLK6-CT-2001-00360), FP6 (SHARE-I3: RII-CT-2006-062193, COMPARE: CIT5-CT-2005-028857, SHARELIFE: CIT4-CT-2006-028812), and FP7 (SHARE-PREP: N°211909, SHARE-LEAP: N°227822, SHARE M4: N°261982). Additional funding from the German Ministry of Education and Research, the Max Planck Society for the Advancement of Science, the U.S. National Institute on Aging (U01_AG09740-13S2, P01_AG005842, P01_AG08291, P30_AG12815, R21_AG025169, Y1-AG-4553-01, IAG_BSR06-11, OGHA_04-064, HHSN271201300071C) and from various national funding sources is gratefully acknowledged (see www.share-project.org).This article uses data from the generated Job Episodes Panel (Orso et al. 2016; for methodological details, see Antonova et al. 2014; Brugiavini et al. 2013). The Job Episodes Panel release 5.0.0 is based on SHARE Waves 1, 2, and 3 (SHARELIFE) (Börsch-Supan 2017a; 2017b; 2017c).

I generated four variables containing annual information on four dimensions of family life: (1) whether respondents were living in the parental home, (2) were cohabiting, or (3) were married, and (4) the timing of childbirths and adoptions. I then constructed sequences from age 15 to 50, thereby capturing not only early family formation, such as first marriage and childbirth, but also later family formation events, such as divorce and remarriage. An age range of 35 years is also much longer than in recent research with family trajectories (e.g., Elzinga & Liefbroer 2007; Fasang & Raab 2014).

Sequences are composed of 35 consecutive annual states. The results displayed in this study use a simplified state definition.[9] Each sequence state is (1) in the parental home, (2) single, (3) cohabiting, or (4) married. Further, each state element can be extended by the presence of at least one child: for example, married with at least one child. (See Table 3 in the appendix for a comprehensive overview.) Note that "single" indicates that the respondent was neither in the parental home nor cohabitating; it does not specify the relationship status of the respondent. Full information is available for 22,272 individuals (see Table 4 in the appendix for case sizes by birth cohort and country). I present results using birth cohorts in three-year groups from 1924–1926 to 1954–1956.

Measuring Differentiation as Sequence Complexity

This study aims to describe family life course differentiation across birth cohorts and countries. I use a composite measure developed in sequence analysis that corresponds with the life course concept of differentiation: the sequence complexity index. This index measures variability within sequences as the geometric mean of normalized sequence transitions and normalized longitudinal sequence entropy (Gabadinho et al. 2010; 2011). Formally, the complexity, C, of a sequence, x, is defined as follows:

$$C(x) = 100 * \sqrt{\frac{q(x)}{q_{max}} * \frac{h(x)}{h_{max}}}, \qquad (1)$$

where the number of transitions within a sequence, $q(x)$, is divided by the theoretical maximum number of transitions possible, q_{max}; the longitudinal entropy of a sequence, $h(x)$, is divided by the theoretical maximum, h_{max}.

[9] I performed the analyses with different sequence state definitions to ensure that the results are not dependent on the sequence alphabet. The results are robust to more differentiated sequence state definitions.

Formally, longitudinal sequence entropy is

$$h(x) = -\sum_i^s \pi_i log\pi_i, \qquad (1.1)$$

where π is the proportion of occurrences in a given state, i, of the sequence alphabet, s. Entropy within sequences is maximal when each state occurs an equal number of times, which reflects that the unpredictability of a given state is maximal. Complexity is minimal in sequences composed of a single state and maximal in sequences that contain each state element with equal durations and have the maximum number of transitions. The complexity index provides a more nuanced indicator of life course differentiation compared with just the number of transitions or distinct states because the degree of uncertainty within life courses is incorporated through sequence entropy.

Figure 1: Artificial Example of Family Trajectories and Sequence Complexity

Family Trajectory 1: $C(x)$ = 46.213

P	P	S	S	M	M	MC	MC	MC	MC

Family Trajectory 2: $C(x)$ = 58.648

P	P	S	S	C	C	M	M	MC	MC

Family Trajectory 3: $C(x)$ = 51.215

P	S	C	M	MC	MC	MC	MC	MC	MC
t_1	t_2	t_3	t_4	t_5	t_6	t_7	t_8	t_9	t_{10}

As an example, consider the three artificial family trajectories in Fig. 1. (See the appendix for the calculation of sequence complexity in Fig. 1.) The first sequence, composed of two parental home states (P), two single states (S), two married states (M) followed by four married with children states (MC), has a lower complexity value than sequences 2 and 3. Sequences 2 and 3 have an additional transition into (or out of) cohabitation, which makes them more complex than Sequence 1. Sequences 2 and 3 differ in regard to the duration spent in distinct states and thus in regard to the degree of predictability displayed by the sequences. Although the second sequence is characterized by frequent transitions, the third sequence shows high stability within the state married with children. Therefore, the complexity of Sequence 3 is lower than that of Sequence 2 because the longitudinal entropy (i.e., the degree of unpredictability) of the third sequence is lower.

Covariates

I introduce individual-level characteristics in the cross-classified models (discussed shortly) that were theorized to be related to family formation complexity: educational attainment, socioeconomic status, and gender. Educational attainment is operationalized using the ISCED 1997 scale recoded as (1) no formal education, (2) preprimary, (3) primary, (4) secondary, and (5) postsecondary education. I use two socioeconomic status indicators that either precede or occur early in individuals' active family formation phase. First, I use the occupation of the main breadwinner when the respondent was age 10 using the reduced ISCO88 scale as a proxy for childhood socioeconomic status. Even though occupation is not equivalent to socioeconomic condition or social class, it is an approximation. Second, whether the respondent's first employment was in the public or private sector serves as a proxy for the stability of employment and amount of benefits available during the early phase of family formation.

Modeling Sequence Complexity

I use a cross-classified random-effects approach to analyze how family trajectories vary across countries and across birth cohorts, and whether they vary more across countries or cohorts. This enables me not only to investigate levels of family trajectory complexity across countries and cohorts but also to decompose the proportion of family trajectory complexity variance attributable to countries and to cohorts. These models represent a special case of multilevel modeling in which the higher-level units cannot be hierarchically ordered (Rabe-Hesketh & Skrondal 2012, pp.433–460; Snijders & Bosker 2012, pp.155–165). Individuals are cross-classified by birth cohort membership and country of residence. Formally, sequence complexity is modeled as follows:

$$y_{ijk} = \beta_0 + \zeta_j + \zeta_k + \zeta_{jk} + \varepsilon_{ijk}, \qquad (2)$$

where the sequence complexity, y_{ijk}, is composed of the constant β_0 (i.e., the grand mean); the group-specific error terms, ζ_j, ζ_k, and ζ_{jk}; and the individual error term, ε_{ijk}.[10] The variance attributable to countries and birth cohorts is identified through country- and birth cohort–specific deviations from the grand mean, ζ_j and ζ_k, respectively. The group-specific deviations from the constant are also referred to as random intercepts or effects. Change caused by universal trends that affect cohorts identically across all countries will be captured in the cohort-

[10] The models are estimated using restricted maximum likelihood estimates (REML) and identity covariance matrices.

specific deviations, whereas country-specific differences across all cohorts will be captured by the country-specific deviations. To capture country-specific change across birth cohorts, the additive cross-classified model is extended through an interacted random effect, ζ_{jk}.[11] The relative proportion of complexity variance that is accountable to country- or birth cohort–specific differences are calculated as intraclass correlation coefficients (ICC), ρ:

$$Var(y_{ijk}) = Var(\zeta_j + \zeta_k + \zeta_{jk} + \varepsilon_{ijk}) = \psi_j + \psi_k + \psi_{jk} + \sigma, \tag{2a}$$

$$\rho_{Country} = \frac{\psi_j}{\psi_j + \psi_k + \psi_{jk} + \sigma} \tag{2b}$$

and alternatively

$$\rho_{Cohort} = \frac{\psi_k}{\psi_j + \psi_{k+}\psi_{jk} + \sigma}, \tag{2c}$$

where σ is the constant variance of the Level 1 residuals; and ψ_j, ψ_k, and ψ_{jk} are the variances of the country-specific, cohort-specific, and interacted random intercepts, respectively, of the parameters in Eq. (2)**.** Equation (2b) calculates the correlation of observations from the same country but different cohorts by dividing the country-specific variance by the total variance. Likewise, Eq. (2c) calculates the correlation of observations from the same cohort but different countries.

Cross-classified random-effects regressions can also be estimated with covariates. In this case, sequence complexity is modeled as follows:

$$y_{ijk} = \beta_0 + \boldsymbol{X}_{ij}\boldsymbol{\beta} + \zeta_j + \zeta_k + \zeta_{jk} + \varepsilon_{ijk}, \tag{3}$$

where $\mathbf{X}_{ij}\boldsymbol{\beta}$ contains the covariates and their coefficients. Similar to linear multilevel models with hierarchically nested random effects, the reduction of country-specific and cohort-specific variation by the covariates can be calculated as a pseudo-R^2:

$$R^2{}_{Country} = \frac{\psi_j - \psi_{j,C}}{\psi_j + \psi_k + \psi_{jk} + \sigma} \tag{3.1}$$

and alternatively

[11] Shi et al. (2010) recommended that researchers include random interaction effects because their simulations and empirical tests showed that higher-level random-effects estimates are biased if significant interacted crossed factors are omitted.

$$R^2_{Cohort} = \frac{\psi_k - \psi_{k,C}}{\psi_j + \psi_{k+}\psi_{jk} + \sigma}, \tag{3.2}$$

where the variance component of the conditional model is denoted with the subscript C. The standard assumptions for random-effects multilevel modeling apply and are clearly stated and examined in Online Resource 1 (see the upcoming section, Discussion and Conclusion). I conclude that the model parameters are generally consistently and efficiently estimated.

Overview of the Analytical Strategy

My analytical strategy entails four steps.[12] First, I address my first two research questions: how family trajectories vary across birth cohorts, and how they vary across countries. To do this, I estimate unconditional cross-classified random-effects regressions on sequence complexity and investigate the country and birth cohort averages using empirical Bayes predictions of the random effects, ζ_j and ζ_k, and their standard errors (Rabe-Hesketh & Skrondal 2012, pp.109–114). Comparing empirical Bayes predictions of the country- and cohort-specific complexity intercepts is better than comparing ordinary least squares (OLS) estimates because information is weighted by its reliability.[13] Examining the empirical Bayes estimates allows me to test whether levels of family trajectory complexity have increased across birth cohorts (H1) and whether they are highest in Scandinavian countries, followed by continental European countries, and lowest in southern and eastern Europe (H2). I additionally analyze the empirical Bayes predictions of the interacted random intercepts, which indicate the average deviations of countries from the birth cohort random intercepts. If significant deviations exist, I can conclude that family trajectory variation across time is country-specific (H3).

Second, I address my third and core research question: whether family trajectories vary more across countries or across birth cohorts. I calculate the country and birth cohort intraclass correlation coefficients for both the unconditional and conditional cross-classified models, which enables me to enumerate the proportions of complexity variance attributable to countries and to cohorts. If the intraclass correlation coefficients are higher for countries than cohorts, my expectation that cross-national variation is larger than cross-temporal variation (H4) is

[12] I use the *TraMineR* (Gabadinho et al. 2011) package to calculate sequence complexities and the *WeightedCluster* (Studer 2013) package to perform cluster analyses on the sequence-based distance matrixes in R, version 3.2.0. The cross-classified regressions are calculated using the mixed command in STATA, version 14.

[13] Country, cohort, and country-cohort balanced panels were generated and analyzed to test the robustness of the empirical Bayes predictions (i.e., predictions without reliability coefficients). The results do not change substantially and lead to the same substantive conclusions.

validated. As a third step, I then estimate conditional cross-classified models by introducing educational attainment, socioeconomic status, and gender as covariates.

Finally, I use results from cluster analysis to illuminate the qualitative differences between family life courses within countries and birth cohorts that underlie the regression results. In addition, I show that sequence complexity is a valid construct for life course differentiation. Specifically, I analyze complexity distributions within family trajectory clusters and describe how these differ across Europe and across birth cohorts as well as across gender, educational attainment, and socioeconomic status. Combining sequence and cluster analysis is a common method to inductively establish common trajectory patterns or groups (see Aisenbrey & Fasang 2010). I calculate a pairwise sequence distances matrix using optimal matching. This distance matrix is then subjected to a Ward cluster analysis, a hierarchal clustering method that minimizes the residual variance to establish groups with low within-group distance and high between-group distance.

I rely on the average silhouette width (ASW) to determine the optimal number of clusters. The ASW is calculated by computing the silhouette of each observation—that is, how close an observation is to the observations within its own cluster compared with how close it is to the observations in other clusters, then averaging the silhouettes within each cluster, and finally averaging the cluster specific silhouette values. Kaufman and Rousseeuw (1990, p.88) proposed an interpretation of ASW values, where 0.25–0.50 denotes weak structure, 0.51–0.75 indicates a reasonable structure, and 0.76–1.0 is a strong structure indicating clearcut clusters in the data. Cluster solution quality measures displayed in Section 8 in Online Resource 1 indicate that family trajectories are reasonably well structured into family patterns involving marriage as well as parenthood and those following different pathways. The two-cluster solution (ASW = 0.61) reveals variation in family trajectories across countries and across birth cohorts, but it masks important differences because diverse family trajectories are "dumped" together into one cluster. Therefore, I discuss the second-best solution with six clusters (ASW = 0.29) in the following section.

Results

Family Trajectory Differentiation

The unconditional cross-classified random-effects regression results for family trajectory complexity are presented in columns 1 and 2 of Table 1. The first model, column 1, excludes the interacted random effect. The results of the conditional model on sequence complexity are displayed in column 3 of Table 1. I first describe how family trajectories vary across birth cohorts and countries using empirical Bayes predictions of random intercepts from Model 2 (see Table 1, column 2) shown in Fig. 2.

Table 1: Cross-Classified Random Effects Regression on Sequence Complexity

	Unconditional Additive 1	Unconditional Interacted 2	Conditional Interacted 3
Female			–0.570***
			(0.071)
Education (ref. = secondary)			
None			–0.802***
			(0.212)
Preprimary			–0.899***
			(0.106)
Primary			–0.523***
			(0.109)
Postsecondary			1.160***
			(0.103)
Public Sector			0.156
			(0.137)
Occupation of Breadwinner (ref. = agriculture)			
Senior professional			1.301***
			(0.185)
Professional			1.115***
			(0.199)
Technician			1.060***
			(0.184)
Clerk			0.970***
			(0.166)
Service			0.589***
			(0.148)
Craftsman			0.296**
			(0.107)
Industry			0.358*
			(0.176)
Unskilled			0.147
			(0.113)
Armed services			0.592*
			(0.290)
None			0.945**
			(0.289)
Constant	15.063***	15.068***	15.089***
	(0.521)	(0.491)	(0.429)
Var(Cohort)	0.655***	0.584***	0.330***
	(0.301)	(0.284)	(0.170)
Var(Country)	2.942***	2.561***	1.971***
	(1.161)	(1.029)	(0.798)
Var(Interacted)		0.455***	0.456***
		(0.083)	(0.082)
Var(Residual)	28.764***	28.387***	27.512***
	(0.273)	(0.270)	(0.262)

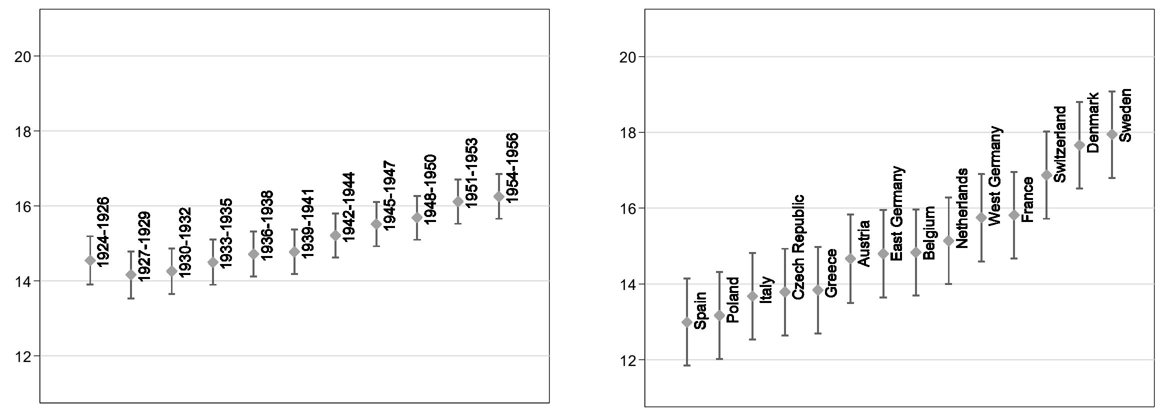
Table 1 continued			
ρ_{Cohort}	2.02	1.82	1.08
$\rho_{Country}$	9.09	8.00	6.51
R^2_{Cohort}			43.60
$R^2_{Country}$			23.03
R^2_{Total}			5.37
N	22,272	22,272	22,272
R Log-Likelihood	–69,064	–68,989	–68,647

Notes: Unstandardized regression coefficients are displayed. Standard errors are shown in parentheses. Significance of random-effect parameters is determined by likelihood-ratio tests. Data are not weighted.
$*p < .05$; $**p < .01$; $***p < .001$

Family trajectories are the least complex in Spain, Poland, and Italy, and they are the most complex in Denmark and Sweden. Family trajectories in East Germany, Belgium, and the Netherlands have average values. With the exception of East Germany and Austria, the empirical Bayes estimates support my expectation that family trajectories are the most complex in Scandinavian social democratic countries, followed by the corporatist continental European countries, with family life courses being the least complex in southern and eastern Europe (H2).

Figure 2 shows a clear trend toward increasing trajectory complexity across birth cohorts; however, it is much less pronounced than expected. The estimated sequence complexity for the birth cohorts 1951–1953 and 1954–1956 are, on average, significantly higher than the cohorts 1939–1941 and older. As expected, the family trajectories of birth cohorts born in the early 1950s are more complex than older birth cohorts (H1).

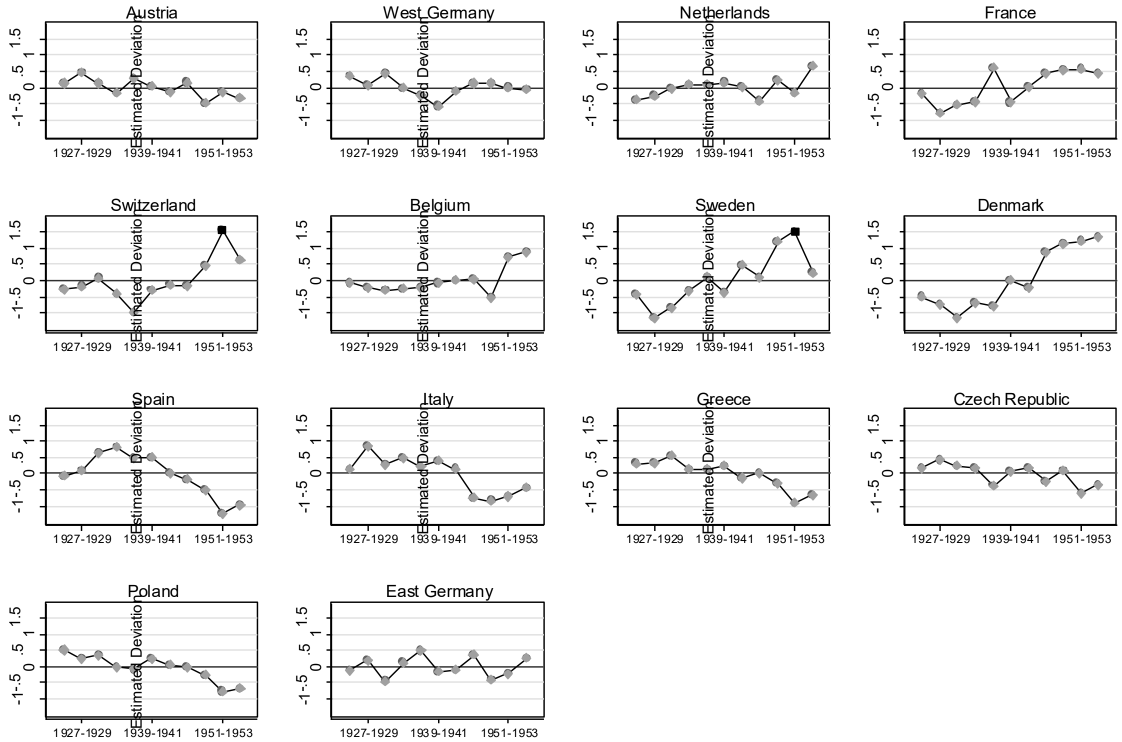
Figure 2: Empirical Bayes Estimates of Mean Sequence Complexity by Cohort and Country



Random intercepts and 95 % confidence intervals are displayed

The significant interacted random effect parameter of column 2 (Table 1) indicates that sequence complexity variation across birth cohorts is not identical in all countries (H3). The country-specific deviations from the birth cohort estimates displayed in Fig. 2 are depicted in Fig. 3. The only statistically significant deviations are found in Switzerland and Sweden for the 1951–1953 cohorts, which have an estimated 1.5 points higher average complexity than the general trend. This indicates that levels of family life course complexity began to increase earlier in Sweden and Switzerland, most likely associated with an early shift toward prolonged family formation involving periods of cohabitation or independent living before marriage in these two countries. All other countries display no significant deviations from the estimated general trend. Despite some country-specific time trends, the results demonstrate an unexpected level of persistent cross-national differences with common trends of increasing complexity.

Figure 3: Empirical Bayes Estimates of Country-Specific Deviations from Mean Birth Cohort Complexity.



Note: Random intercepts displayed
Black denotes significant deviations; p<0.05

I now turn to partitioning the sequence complexity variance between countries and birth cohorts using cross-classified random-effects modeling. As expected, the results demonstrate that the complexity of family trajectories varies more across countries than across birth cohorts (H4). The unconditional average of family trajectory complexity is 15, as indicated by the constant in columns 1 and 2 (see Table 1). The country-specific variation from the average is 2.56 and is thus substantially larger than the birth cohort–specific variation estimate of 0.58, displayed under the random effects of Table 1. An estimated 8 % of the family trajectory variance is attributable to country differences, opposed to a marginal 1.8 % accounted for by birth cohort differences, as shown by the intraclass correlations in column 2.

The associations among educational attainment, socioeconomic status, gender, and sequence complexity are displayed in column 3 of Table 1. The family sequences of women are an average of 0.57 points less complex than those of men. Higher educational attainment is significantly associated with more complex family trajectories. Further, family formation is more complex if the main breadwinner of the respondent's childhood household had an occupation requiring a higher skill level than agricultural labor. However, family formation trajectories are also more complex for respondents who had no main breadwinner in their childhood household.[14] The sector of first employment is not significantly associated with sequence complexity. With the exception of the respondent's sector of first employment, these associations are in line with what would be anticipated based on the SDT thesis and institutional arguments of comparative life course sociology.

The conditional intraclass correlations—that is, the proportion of complexity variance attributable to cohort and country differences conditioned on the covariates—also indicate that family trajectories vary considerably more across countries than across birth cohorts when conditioned on the covariates. More than 6.5 % of complexity variation can be attributed to cross-national differences compared with 1 % for differences across birth cohorts. Educational attainment, the occupation of the main breadwinner when the respondent was 10, and gender reduce the country-specific complexity variation by 23 % and the cohort-specific variation by 43.6 %. This indicates that compositional differences account for a considerable amount of complexity variation across countries and cohorts. For example, higher levels of educational attainment in younger cohorts partially account for increasing levels of family formation complexity. These three covariates reduce the total sequence complexity variation by 5.3 %,

[14] This response could mean that there was no main breadwinner or that the main breadwinner had no occupation (e.g., was unemployed).

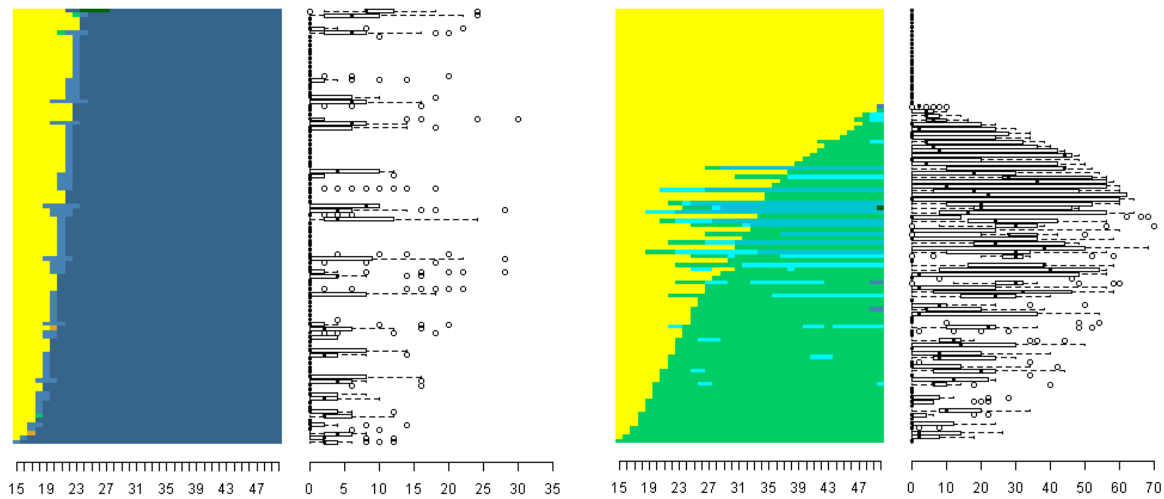
which is considerable for composite sequence metrics (see Biemann et al. 2011; Van Winkle & Fasang 2017).

Family Trajectory Patterns: Results From Exploratory Cluster Analysis

Family life courses can be categorized as (1) early family formation; (2) parental home, single, or cohabitation trajectories; (3) prolonged family formation; (4) union dissolution trajectories; (5) childless marriages; or (6) delayed family formation (see Fig. 4). The family life courses of these clusters are displayed in Fig. 4 as relative frequency sequence plots, which display 100 representative sequences from each cluster on the left and a box plot of the dissimilarities from the respective sequence on the right (Fasang & Liao 2014).[15]

Figure 4: Relative Frequency Sequence Plots of Family Trajectory Patterns

Early Family Formation		**Parental Home, Single, and Cohabitation**	
Sequence Medoids	**Dissimilarities to Medoid**	**Sequence Medoids**	**Dissimilarities to Medoid**



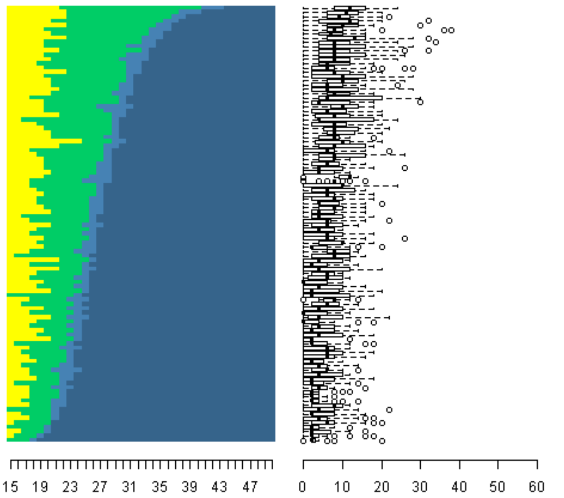
Representation Quality: R^2 = .62 and F = 26.24 **Representation Quality: R^2 = .62 and F = 26.24**

[15] Relative frequency sequence plots are generated by (1) sorting the sequences, (2) dividing the sorted sample into subgroups, (3) choosing medoid sequences from the subgroups to represent them, (4) plotting the medoid sequences, and (5) plotting dissimilarities from the medoid sequences as boxplots with R^2 and F statistics that evaluate the goodness of fit of the chosen medoid sequences. I sort the sequences using multidimensional scaling and divide the sample into 100 medoid sequences. The dissimilarities are calculated using OM distance. The plots were created with the *seqplot.rf* function developed by Matthias Studer, Anette Fasang, and Tim Liao implemented in the *TraMineRextras* package using R, version 3.2.0.

Figure 4 continued

Prolonged Family Formation

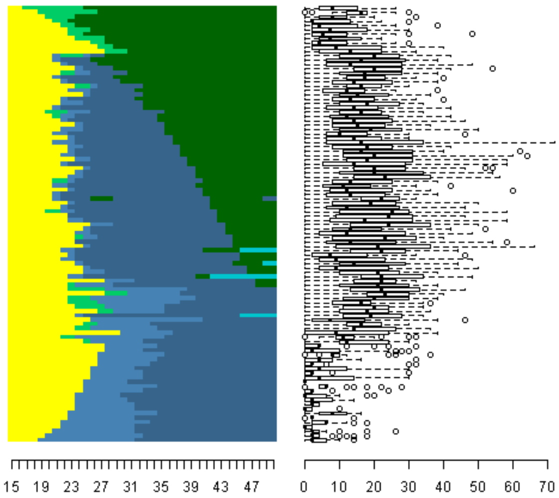
Sequence Medoids **Dissimilarities to Medoid**



Representation Quality: R^2 = .55 and F = 41.71

Union Dissolution

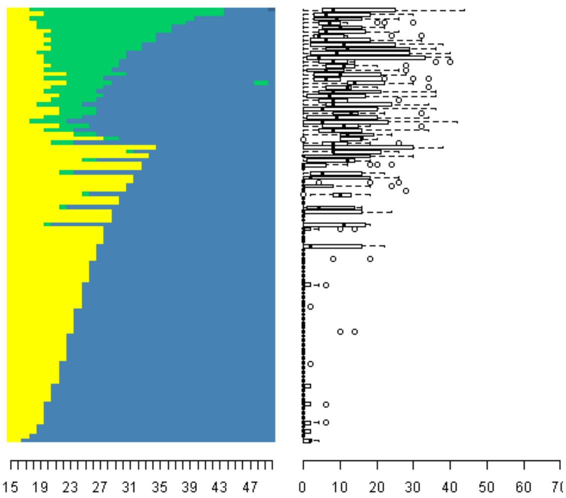
Sequence Medoids **Dissimilarities to Medoid**



Representation Quality: R^2 = .54 and F = 31.86

Childless Marriage

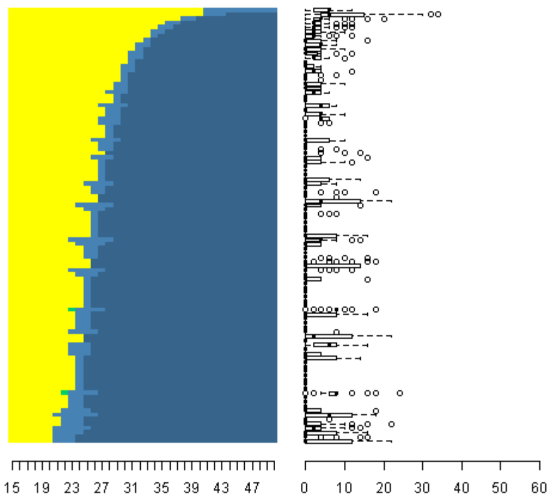
Sequence Medoids **Dissimilarities to Medoid**



Representation Quality: R^2 = .66 and F = 29.54

Delayed Family Formation

Sequence Medoids **Dissimilarities to Medoid**



Representation Quality: R^2 = .84 and F = 495.40

Legend

Parental Home
Cohabiting
Parental Home, Children
Cohabiting, Children
Single
Married
Single, Children
Married, Children

Early and delayed family formation trajectories are characterized by highly coupled transitions out of the parental home into marriage and parenthood by the early to late 20s. Prolonged family formation trajectories are characterized by decoupled transitions in the early life course. A majority lived independently for a period after leaving the parental home before marriage, while some substantially delayed entering parenthood after marriage. Other family trajectories include childless marriages or marriages that dissolved either because of death or because of divorce into independent households or into cohabitation with children. A final cluster includes trajectories that consist of independent living, of cohabitation, or of living in the parental home.

The distribution of sequence complexity within the clusters as well as the cluster sizes are displayed in Table 2. The early and delayed family formation clusters are the largest, each incorporating approximately 30 % of family trajectories. Delayed family trajectories are slightly more complex than early family trajectories because there is less state stability within marriage with children resulting from a longer duration in the parental home. The highest complexity averages are found within the prolonged family formation and union dissolution clusters because trajectories within these clusters include an additional transition into a single state out of the parental home or out of marriage.

Table 2: Distribution of Sequence Complexity by Family Trajectory Clusters

	Early Family Formation	Parental Home, Single, and Cohabitation	Prolonged Family Formation	Union Dissolution	Childless Marriage	Delayed Family Formation	Total
Complexity	12.51	12.29	19.87	22.40	12.76	14.72	15.51
(SD)	(3.48)	(8.48)	(4.61)	(6.41)	(5.69)	(2.46)	(5.66)
N	6,034	1,473	3,161	2,524	1,381	7,699	22,272
(%)	(28.38)	(5.97)	(14.96)	(11.87)	(6.16)	(32.66)	(100.00)

Notes: Means, percentages, and standard deviations (in parentheses) are displayed. Data are weighted

The prevalence of the different family formation patterns varies across countries in a manner consistent with the regression results. The distribution of family trajectory patterns within countries and cohorts is displayed in Table 5 in the appendix. Levels of differentiation are the highest in Sweden and Denmark because early and delayed family formation trajectories are underrepresented in these countries while prolonged family formation and union dissolution trajectories are overrepresented. Low levels of differentiation in the Czech Republic and Poland are associated with the dominance of early family formation trajectories. Similarly, a dominance of delayed family formation trajectories in Spain, Italy, and Greece account for low levels of differentiation in southern Europe.

Consistent with the regression results, the prevalence of the distinct family trajectory patterns varies little between birth cohorts. Although early family formation trajectories became somewhat more common between 1924–1926 and 1954–1956, delayed family trajectories became considerably less common. Prolonged family formation and childless marriage trajectories remained at a relatively constant level, but the parental home, single, or cohabitation as well as union dissolution patterns became more prevalent. Levels of differentiation for the 1951–1953 and 1954–1956 cohorts are slightly higher because delayed family formation patterns decreased while patterns involving divorce increased. The distribution of family formation patterns across countries and across birth cohorts is in line with the SDT and comparative life course sociology.

The distribution of gender, educational attainment, and socioeconomic status across family trajectory clusters is also consistent with the regression results (see Table 6 in Appendix). Although women are overrepresented in the early family formation cluster, men delay family formation, which corresponds to the finding that women's family life courses are somewhat less complex than men's. The educational gradient in family trajectory complexity is likely attributable to individuals with primary education following early and delayed patterns of family formation while individuals with postsecondary education commonly form independent households before marrying. This pattern can also be observed among individuals whose main breadwinner during childhood was in the professional occupational classes rather than in the agricultural sector.

Sensitivity Analyses

I conduct multiple sensitivity analyses to test the robustness of my results. The first set of robustness checks addresses the question whether complexity would vary more across cohorts relative to countries if I would observe younger cohorts born after 1956. Unfortunately, no other suitable data sets exist that would allow me to analyze the family formation trajectories of men and women aged 15–50 for cohorts born after 1956.[16] I nonetheless replicate my analyses using the Harmonized Histories data from the Generations and Gender Programme (U.N.E.C. 2005;

[16] Although the Generations and Gender Programme has extremely rich life history data on a number of countries, using them would only extend the cohort range past 1956 for Poland, Belgium, and Sweden for long life trajectories. An alternative data source would be the 2006 European Social Survey used by Hofäcker and Chaloupková (2014) to analyze family formation trajectories across 23 European countries for those aged 18–35; however, these data would not expand the cohort range of individuals observed until age 50. Moreover, the 2006 European Social Survey did not collect information on the timing of divorce, which is necessary when analyzing family life courses until age 50.

Perelli-Harris et al. 2010) with trajectories of individuals aged 15–35 for cohorts born between 1939–1971 from 13 European countries. I find that differences across cohort are still small compared with cross-national differences and in some cases are even smaller than in the analysis presented earlier (see Section 4 in Online Resource 1 for more details). The results solidify my conclusion that the increase in family trajectory complexity is still minor even if the cohort range is extended beyond 1956. Further, the analyses demonstrating even smaller cross-temporal variation using shorter trajectories underline the importance of using long family life courses when analyzing change partially due to events in later life (e.g., divorce and remarriage).

The second set of sensitivity analyses pertain to the dependent variable—sequence complexity—and its influence on the results. First, I conduct separate analyses on entropy, the number of transitions as well as logarithmic complexity and its components. The results are substantively similar and lead to the same conclusions (see Section 1 in Online Resource 1). Second, I perform robustness checks on complexity weighted by durations in specific sequence states. Although the results are quite similar to those presented earlier, cross-national differences are inflated when complexity is weighted to give more importance to durations of being single without children, and gender differences become larger when weighted by durations spent in the parental home with children or single with children (see Section 2 in Online Resource 1).

A final set of sensitivity analyses examines how model specifications influence the results. I estimated models with yearly, two-year, four-year, and five-year cohorts rather than three-year cohorts used in the analyses earlier. The results are highly robust to different cohort groupings (see Section 3 in Online Resource 1). As another robustness test, I analyze two-level models with country-cohort clusters, which indicate that the intraclass correlation coefficients from the cross-classified models are well estimated (see Section 7 in Online Resource 1). Finally, I conduct sensitivity analyses omitting single countries and cohorts that demonstrate that my results are not driven by a single country or cohort (see Section 5 in Online Resource 1).

Discussion and Conclusion

I set out to ascertain (1) how family trajectories vary over time, (2) how they vary across countries, and (3) whether they vary more across time or across countries. These questions are motivated by two research traditions in the field of comparative family demography and sociology: the ideational account of the SDT (Lesthaeghe & Van de Kaa 1986) and the institutional account of comparative life course sociology (Mayer 1997; 2009). Based on these theoretical perspectives, I hypothesized that family trajectories became more differentiated across cohorts (H1) and that family trajectories within social democratic countries are the most differentiated, followed by corporatist countries, and are the lowest within southern and eastern European countries (H2). Finally, I argued that the speed and extent of change in family formation within countries result from an interaction between the dissemination of postmaterialism and the implementation of defamilizing institutions. It follows that change over time is country-specific (H3) and that cross-national variation is larger than cross-temporal variation (H4). All four hypotheses were supported by the empirical results, although I observed a higher level of contemporaneous change across countries than expected.

The analyses presented have various potential limitations. The SHARELIFE data were collected retrospectively from elderly respondents, posing the problem of recall error. Havari and Mazzonna (2015) compared information collected in the SHARELIFE childhood circumstances module with national registry data and concluded that recall error does not compromise the validity or usefulness of the data. Further, the life history calendar used in SHARELIFE collected data on an annual rather than monthly basis. Both recall error and the coarseness of annual life history data may cause an underestimation of family life course differentiation, especially in the early cohorts and in countries with high differentiation levels.

Another potential limitation lies within the birth cohorts analyzed as well as the clustering of cohorts and countries. The data lack birth cohorts entering family formation at the dawn of the twentieth century and after the 1980s, which could display considerably higher levels of family trajectory differentiation. Even with the relatively large number of birth cohorts and countries included in this study, the estimated variance components may be biased downward because of small cluster sizes (Bryan & Jenkins 2015). All these limitations, if anything, point to a potential underestimation of the true degree of differentiation in family life courses. Therefore, the analyses can be understood as lower-bound estimates. The finding of a strong influence of institutional path dependency on family life courses suggests that cross-temporal variation will probably not outweigh cross-national differences for decades to come, although this is an empirical question.

One of my main contributions to the literature is the introduction of a novel methodological approach that simultaneously quantifies cross-national and cross-temporal variation in family life courses. This methodological approach is important for three reasons. First, it enables family demographers and sociologists to describe the extent of increasing family formation complexity by using cross-national differences as a point of reference. I demonstrated that the extent of change in family formation is often overstated in light of much more substantial variation across European countries. Second, this approach addresses two theoretical accounts of family life course variation and enables family demographers and sociologists to investigate processes of family formation without neglecting either the temporal or spatial dimension. For example, I demonstrated that educational attainment is associated with family formation complexity and that compositional differences in educational attainment account for both cross-national and cross-temporal variation. Third, my methodological approach is applicable to other areas of research on the temporal and spatial variation of process outcomes, such as democratic consolidation or health histories.

The implications of my results both advance the SDT thesis and substantiate previous research. I bring a long generational perspective into the debate on increasing complexity in family formation by integrating the theoretical perspectives of the SDT and comparative life course sociology with a focus on temporal order. This is important to gain a deeper understanding of how family formation differentiation engendered by the dissemination of postmaterialism over time can be inhibited by national institutional arrangements that lag this cultural change. For example, although studies have demonstrated that the dissemination of postmaterialism developed similarly in Denmark and the Netherlands (e.g., Inglehart & Abramson 1994), defamilizing institutions (such as maternity and paternal leave as well as early childcare) that facilitate high female labor market participation were introduced much later or not at all in the Netherlands. Although defamilization lowered the risks of complex family formation associated with postmaterialism in Denmark, continued familization and gendered decommodification in the Netherlands further incentivize early marriage and parenthood, especially for women. This process of institutional lag and the suppression of family formation differentiation is likely to continue in continental Europe and also in southern and eastern Europe.

More generally, my study underlines large and relatively stable cross-national differences in levels of family life course differentiation. This supports the notion that “societies change very gradually” (Mayer 2005, p.17) and that path dependency in institutions may be the primary source of gradual change in family life courses. Many of the cross-national differences and changes across cohorts are consistent with the comparative life course literature as well as the SDT thesis. Future research should further investigate how ideational and institutional change jointly unfolds over time to shape family life courses and how these trends may be associated with social inequality.

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Appendix

Table A3: List of Sequence State Elements and Average Durations

State Abbreviation	State Definition	Average State Duration (years)
P	In the parental home and without children	8.487
PC	In the parental home with at least one child	0.091
S	Outside the parental home, not cohabitating with an intimate partner, and without children	2.103
SC	Outside the parental home, not cohabitating with an intimate partner, and with at least one child	1.023
C	Cohabitating with an intimate partner without children	0.234
CC	Cohabitating with an intimate partner with at least one child	0.370
M	Married without children	3.337
MC	Married with at least one child	20.354

Table A4: Sample Frequencies Cross-Classified by Country and Birth Cohort

	24–26	27–29	30–32	33–35	36–38	39–41	42–44	45–47	48–50	51–53	54–56	Total
Austria	22	59	49	65	72	119	112	95	87	77	32	789
West Germany	45	57	61	83	132	168	154	113	168	177	95	1,253
Sweden	77	84	106	138	159	197	218	239	193	167	69	1,647
Netherlands	53	70	91	132	141	181	228	281	263	240	183	1,863
Spain	63	100	131	168	126	146	138	157	153	162	152	1,496
Italy	56	77	140	158	209	238	219	232	237	181	170	1,917
France	73	119	135	151	150	174	192	233	276	250	231	1,984
Denmark	75	91	118	122	132	155	207	234	222	217	289	1,862
Greece	70	75	136	174	168	156	193	241	267	321	199	2,000
Switzerland	43	59	77	82	97	93	133	135	124	122	132	1,097
Belgium	102	119	168	183	189	194	237	264	308	294	248	2,306
Czech Republic	47	53	102	111	117	165	202	215	211	188	162	1,573
Poland	43	63	88	79	120	115	122	189	209	222	228	1,478
East Germany	29	38	47	73	95	108	120	126	132	136	103	1,007
Total	798	1,064	1,449	1,719	1,907	2,209	2,475	2,754	2,850	2,754	2,293	22,272

Table A5: Descriptive Statistics on the Study Countries and Birth Cohorts by Cluster Grouping

	Early Family Formation	Parental Home, Single and Cohabitation	Prolonged Family Formation	Union Dissolution	Childless Marriage	Delayed Family Formation
Countries						
Austria	33.84	6.97	15.21	15.08	7.35	21.55
West Germany	27.11	3.87	19.50	9.70	7.15	32.67
Sweden	22.37	7.29	32.33	13.90	5.34	18.77
Netherlands	21.27	5.24	13.22	13.32	8.95	38.00
Spain	22.38	7.65	3.13	4.98	5.78	56.08
Italy	23.99	4.22	6.42	5.83	4.92	54.62
France	27.65	8.01	17.71	15.06	5.82	25.75
Denmark	22.44	6.49	37.07	13.45	6.85	13.71
Greece	17.23	7.53	7.31	6.64	7.80	53.49
Switzerland	17.38	10.11	23.62	13.72	7.60	27.56
Belgium	30.51	5.79	3.72	14.03	6.07	39.89
Czech Republic	48.60	2.63	1.42	10.87	3.96	32.52
Poland	47.25	2.38	7.71	4.79	4.62	33.25
East Germany	22.63	6.18	24.40	6.52	4.61	35.66
Birth Cohorts						
1924-1926	21.99	5.61	16.53	7.81	9.39	38.68
1927-1929	23.33	6.18	14.23	8.15	7.72	40.39
1930-1932	28.99	4.56	13.21	5.57	6.21	41.46
1933-1935	24.65	5.11	13.04	9.23	6.23	41.73
1936-1938	26.30	5.22	16.07	9.41	7.41	35.60
1939-1941	30.15	4.41	17.27	10.70	5.26	32.21
1942-1944	28.84	6.31	15.86	12.30	5.86	30.82
1945-1947	29.15	5.51	14.47	13.03	5.12	32.72
1948-1950	30.94	6.34	14.36	15.27	5.00	28.08
1951-1953	29.12	7.43	15.04	14.21	7.33	26.88
1954-1956	29.63	7.61	14.40	14.86	5.83	27.67
Total	28.38	5.97	14.96	11.87	6.16	32.66

Notes: Row percentages are displayed. Data are weighted.

Table A6: Summary Statistics by Cluster Grouping

	Early Family Formation	Parental Home, Single and Cohabitation	Prolonged Family Formation	Union Dissolution	Childless Marriage	Delayed Family Formation
Gender						
Male	18.17	6.71	15.97	10.92	6.06	42.16
Female	37.90	5.27	14.01	12.75	6.25	23.81
Education						
None	32.30	6.05	5.36	7.16	5.42	43.72
Preprimary	35.48	5.39	10.54	8.73	6.26	33.60
Primary	36.14	5.18	7.97	11.93	6.05	32.73
Secondary	27.48	5.75	16.11	12.93	6.20	31.52
Postsecondary	14.87	7.60	25.35	13.75	6.19	32.25
Sector of First Employment						
Private	29.26	5.85	14.71	11.82	6.10	32.27
Public	19.74	7.17	17.37	12.36	6.77	36.58
Occupation of Breadwinner						
Senior professional	17.65	8.28	26.34	15.06	7.02	25.66
Professional	16.03	8.91	24.82	13.80	7.70	28.73
Technician	25.78	6.40	15.53	15.22	7.60	29.46
Clerk	23.01	6.64	12.66	14.88	6.06	36.76
Service	25.77	5.08	16.12	13.50	7.32	32.21
Agriculture	26.45	6.05	18.69	7.97	5.31	35.53
Craftsman	31.44	5.28	11.48	12.51	6.05	33.24
Industry	33.93	5.38	10.73	12.09	6.57	31.30
Unskilled	34.40	5.65	10.46	12.10	5.73	31.66
Armed services	24.09	6.96	14.38	13.01	8.13	33.43
None	38.51	5.02	10.85	14.90	5.51	25.21
Total	28.38	5.97	14.96	11.87	6.16	32.66

Notes: Row percentages are displayed. Data are weighted.

Calculation of Sequence Complexity for Figure 1

I. Maximum Longitudinal Entropy

Calculation for maximum entropy of a sequence with 10 consecutive states and 8 possible sequence elements. An equal occurrence of each state element implies that each element is observed 1.25 times.

$$h_{max} = -\left[10 * \left(\frac{1.25}{10} log \frac{1.25}{10}\right)\right]$$

$$= 2.079$$

II. Family Trajectory 1: P/2 S/2 M/2 MC/4

$$h(x) = -\left[3 * \left(\frac{2}{10} log \frac{2}{10}\right) + \left(\frac{4}{10} log \frac{4}{10}\right)\right]$$

$$= 1.332$$

$$C(x) = 100 * \sqrt{\frac{3}{9} * \frac{1.332}{2.079}}$$

$$= 46.213$$

III. Family Trajectory 2: P/2 S/2 C/2 M/2 MC/2

$$h(x) = -\left[5 * \left(\frac{2}{10} log \frac{2}{10}\right)\right]$$

$$= 1.609$$

$$C(x) = 100 * \sqrt{\frac{4}{9} * \frac{1.609}{2.079}}$$

$$= 58.648$$

IV. Family Trajectory 3: P/1 S/1 C/1 M/1 MC/6

$$h(x) = -\left[4 * \left(\frac{1}{10} log \frac{1}{10}\right) + \left(\frac{6}{10} log \frac{6}{10}\right)\right]$$

$$= 1.227$$

$$C(x) = 100 * \sqrt{\frac{4}{9} * \frac{1.227}{2.079}}$$

$$= 51.215$$

CHAPTER 3

Family Polices and Family Life Course Complexity Across 20th Century Europe

The family policy landscape changed dramatically across and within European societies during the 20th century. At the same time, family life courses have become more complex, unstable, and unpredictable. However, there are no empirical studies that attempt to link changes in family policies with increasing family life course complexity. In this study, I address two research questions: 1) what is the association between family policies and family life course complexity and 2) do these associations vary by the life course stage at which individuals experience family policies? Retrospective data from the Survey of Health, Ageing, and Retirement in Europe (SHARELIFE) are used to construct the family life courses of individuals from age 15-50, born 1924-1956, from 15 European countries. I use metrics developed in sequence analysis that incorporate life course transitions and unpredictability to measure the complexity of family formation. Annual policy information from 1924-2008 for each country are combined to generate cohort indices for three policy dimensions: familization, defamilization, and liberalization. These cohort metrics express the policy experiences of individuals over the course of their lives, rather than at a specific historical time point. I find that familization during early and prime adulthood decreases complexity, while defamilization during early adulthood and liberalization during mature adulthood increase complexity. I conclude that family policy reforms may partially account for increasing life course instability and unpredictability across Europe.

Introduction

The European family policy landscape changed dramatically during the 20th century. While most European countries provided little public family support before the recessions of the 1920s and 1930s, state provisions for families increased during the post-war period (Ferrera 2008; Gauthier 1999). Familistic policies, e.g. family allowances, that support a traditional male-breadwinner female-homemaker division of labor were instituted across much of Europe (Saraceno 2016; Leitner 2003). Before the 1970s, defamilizing policies, e.g. public childcare, that aimed to decrease women's dependence on the family were common only in Nordic countries (Cho 2014). Recently, continental European countries began to implement defamilizing policies, which has been described as the "Scandinavization" of European family policy (Mätzke & Ostner 2010; Orloff 2006). Reforms have also aimed at increasing individuals' freedom of choice in family demographic decisions, e.g. the liberalization of divorce laws (Drewianka 2008; González & Viitanen 2009). In sum, European family policy has developed multidimensionally with countries implementing varying degrees of familizing, defamilizing, and liberalizing policies.

Simultaneously, family life courses have become more complex, unstable, and unpredictable across European societies (Buchmann & Kriesi 2011; Billari & Liefbroer 2010). Family policies are assumed to affect family life courses, but no empirical studies have investigated the relationship between policies and the complexity of family trajectories (see Van Winkle 2018 as chapter 2). In this study, I address two research questions: First, what is the association between family policies and family life course complexity? I analyze familizing, defamilizing, and liberalizing policies concurrently, which is important because they can have contradictory impacts on individual behavior. Second, does the timing of family policies within the life course moderate this association? Specifically, I assess whether the associations between policies and complexity vary by the life course stage at which individuals experience family policies. For example, do policies as experienced in young adulthood between age 15-29 have a greater influence on life course complexity than policies as experienced during prime adulthood between age 30-39 and mature adulthood between age 40-50.

Based on common theoretical approaches in the comparative welfare state and life course sociological literature (Gauthier 2007; Esping-Andersen 1990; 1999; Mayer 1997; 2004), I formulate four hypotheses (see chapter 1): First, I expect that *familizing policies are associated with less complex family trajectories* (H1), because they actively or implicitly incentivize early marriage and parenthood (Leitner 2003; Saraceno 2016). Second, as defamilizing policies decrease the opportunity costs involved with divorce and nonmarital childbirth, I assume that *defamilizing policies are associated with more complex family trajectories* (H2) (Lister 1994; Esping-Andersen 1999; Kröger 2011; Lohmann & Zagel 2016). Third, it is likely that *liberalizing family policies are associated with more complex family trajectories* (H3), for example, because liberal divorce legislation may increase marriage, divorce and remarriage (Becker et al. 1977; Alesina & Giuliano 2006). Finally, institutional influences on individuals' life courses depends on the timing of those influences (Elder et al. 2003). Early experiences are likely most influential, because their effects can be path dependent and cumulative (Dannefer 2003). Therefore, I contend that *the experience of familizing, defamilizing, and liberalizing family policies during early adulthood will have a greater influence on the complexity of family trajectories than experiences during prime or mature adulthood* (H4).

Data & Methods

Sample & Sequence Definition

I use SHARELIFE (Börsch-Supan et al. 2013; Schröder 2011) to test my hypotheses.[17] The SHARELIFE life history data allow me to study family life courses holistically as process outcomes, incorporating distinct events as well as their durations and their sequencing (Abbott 2005b). It is important to study family formation as a trajectory rather than a series of indicators, because family life courses may be similar in one respect, e.g. cohabitation before marriage, but different in others, e.g. the timing of marriage and duration of being married without children. Looking at only one of these markers will give an incomplete picture of the differences and similarities in family life courses.

My sample consists of respondents age 50 and older as well as their partners from 15 European countries born 1924-1956. I combine residential, union, and fertility information to operationalize individuals' family trajectories as sequences that consist of annual states from age 15-50. Sequence states can either be living with parents, single, cohabiting, married, or

[17] This article uses data from SHARE Waves 1, 2, and 3 (SHARELIFE) (Borsch-Supan 2017a, b, c). See Börsch-Supan et al. (2013) for methodological details. The SHARE data collection has been primarily funded by the European Commission through FP5 (QLK6-CT-2001-00360), FP6 (SHARE-I3: RII-CT-2006-062193, COMPARE: CIT5-CT-2005-028857, SHARELIFE: CIT4-CT-2006-028812), and FP7 (SHARE-PREP: N°211909, SHARE-LEAP: N°227822, SHARE M4: N°261982). Additional funding from the German Ministry of Education and Research, the Max Planck Society for the Advancement of Science, the U.S. National Institute on Aging (U01_AG09740-13S2, P01_AG005842, P01_AG08291, P30_AG12815, R21_AG025169, Y1-AG-4553-01, IAG_BSR06-11, OGHA_04-064, HHSN271201300071C) and from various national funding sources is gratefully acknowledged (see www.share-project.org).This article uses data from the generated Job Episodes Panel (Orso et al. 2016; for methodological details, see Antonova et al. 2014; Brugiavini et al. 2013). The Job Episodes Panel release 5.0.0 is based on SHARE Waves 1, 2, and 3 (SHARELIFE) (Börsch-Supan 2017a; 2017b; 2017c).

divorced; each with or without children. I further differentiate between marriage with one, two, or three or more children. Note that the state single indicates "solo-living", rather than the relationship status of an individual (see Jamieson et al. 2009). Note that the results presented below are robust to more differentiated sequence alphabets, e.g. for higher parity births, and simpler sequences, e.g. no distinction between single and divorce.

Family Policy Indices

To analyze the association between my three policy dimensions and sequence complexity, I construct three cohort indices that express the experiences of individuals during their life course. All indices are created in three steps: First, a country-year dataset is constructed with annual information on family policies for each country from 1924-2008. This long time frame allows me to capture lagged policy effects and as well as policy feedback loops that other studies using short periodic measures might miss. Second, a summary index for each policy dimension is generated. Rather than simple additive indices, I use principle components analysis to empirically produce weighted additive indices. This is important to ensure that no single policy is too dominant based on its empirical range. Third, the country-year indices are averaged for the years a given birth cohort was age 15-50, e.g. the French values from 1939-1974 for a French individual born in 1924. Therefore, the final policy indices are constants for persons from the same country and born in the same year. I also create an early adulthood policy indicator with values averaged from age 15-29, a prime adulthood indicator with values averaged from age 30-39, and a mature adulthood indicator with values averaged from age 40-50.

The familizing policy index is generated using annual information on the availability of unconditional family allowances (Gauthier & Monna 2004) as well as the standardized duration of unpaid parental leave, and parental leave reserved for mothers (DICE 2015). The defamilizing index includes annual information on the availability of public early childcare starting at age 1, public preschool childcare starting at age 3 (Garrouste 2010), and unconditional old age social pensions[18] as well as the standardized duration of paid parental leave, job-protected parental leave, and paternity leave (DICE 2015). Finally, the liberalizing policy index is constructed with annual information on the implementation of divorce by mutual

[18] See the Country Fact Files of HelpAge International: http://www.pension-watch.net/country-fact-file/

consent, no-fault divorce[19], and abortion by request legislation[20]. Note that because of the wide historical range, from 1924-2008, it is difficult to find high quality, detailed, and comparable on a wide range of policy indicators. However, I use the best policy information available to create my indices.

Analytical Strategy

I use country and time fixed effects OLS regression models with pooled standard errors to estimate the associations between my policy indices and sequence complexity. I estimate three models for each policy index: 1) a bivariate model regressing sequence complexity on the policy index, 2) a model adjusted for individual and country-cohort level characteristics, and 3) an adjusted model including all three family policy indices. I include several possibly confounding variables in the models. First, I adjust the models for country-cohort GDP (see Manning 2017; Bolt & van Zanden 2014; Maddison 2003 for comparable GDP measures) and the extent that civil liberties were repressed within country-cohorts (see Coppedge et al. 2017; Pemstein et al. 2017 for the civil liberties repression index). Higher standards of living are associated with more complex family life courses according to the narrative of the Second Demographic Transition thesis (Zaidi & Morgan 2017). However, according to Mills & Blossfeld (2003; 2013), declines in GDP due to recessions may also increase complexity. Life courses in authoritarian regimes to conform to state ideology, which commonly consists of early marriage and parenthood (Lesthaeghe 2010). As highly educated individuals from advantage socioeconomic backgrounds are thought to be the forerunners of the SDT, I additionally control for educational attainment and the occupation of the main breadwinner when the respondent was age 10 (Lesthaeghe & Johan Surkyn 1988). The respondent's gender is also included in the models.

Results

Descriptive Statistics

Average sequence complexity as well as the family policy indices are displayed by birth cohort and country in Figure 2. As can be seen in the upper panel of Figure 2, average sequence complexity has increased across birth cohorts in several countries, most prominently in Sweden,

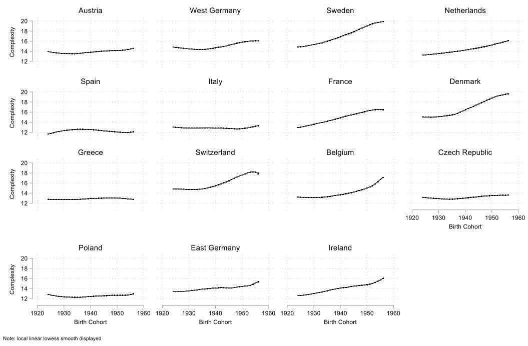
[19]See the Country Reports of Divorce and Maintenance by the Commission of European Family Law: http://ceflonline.net/divorce-maintenance-reports-by-jurisdiction/

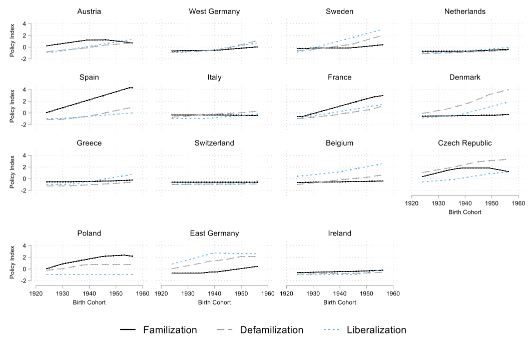
[20]See the United Nations Population Division Department of Economic and Social Affairs Abortion Policies: A Global Review: http://www.un.org/esa/population/publications/abortion/

Denmark, France, Belgium, and Switzerland. However, these increases are relatively minor and, generally, the observed levels of sequence complexity have remained remarkably stable across cohorts. Differences between countries seem to be much larger: complexity levels are highest in Sweden and Denmark and lowest in Poland, Spain and Italy. These descriptive finding are in line with other studies demonstrating that cross-national variation in life courses is substantially larger than cross-temporal variation (Van Winkle 2018; Van Winkle & Fasang 2017).

As can be seen in the lower panel of Figure 2, the levels of familization that cohorts born 1924-1956 experienced during their life course are high and have increased in Spain, France, Poland, and the Czech Republic, while remaining constantly low in the Netherlands, Denmark, and surprisingly Greece. Levels of defamilization generally started low in all countries, but increased to high levels in Denmark, Sweden, East Germany, and the Czech Republic. Similarly, levels of liberalization were low in all countries except East Germany and Belgium, but increased to high levels in Sweden, Denmark, France, and Austria. There is an interesting group of countries – the Netherlands, Italy, Switzerland, and Ireland – that display stable and low levels on all family policy indices. These countries implemented no or only minor family policy reforms until the 1990s. Family policy scholars have described these countries as implicitly familistic or familistic by default, i.e. the Netherlands, Italy, and Switzerland, and as implicitly individualistic or defamilistic through the market, i.e. Ireland, based on their cultural legacies (Lohmann & Zagel 2016; Saraceno 2016). Familization and defamilization are somewhat correlated (r = 0.34), indicating that country-cohorts with high familization levels have slightly higher defamilization levels. While familization and liberalization are not related (r = -0.01), defamilization and liberalization are moderately correlated (r = 0.50).

Figure 1: Average Sequence Complexity and Familizing, Defamilizing, and Liberalizing Policy Indices across Countries and Birth Cohorts

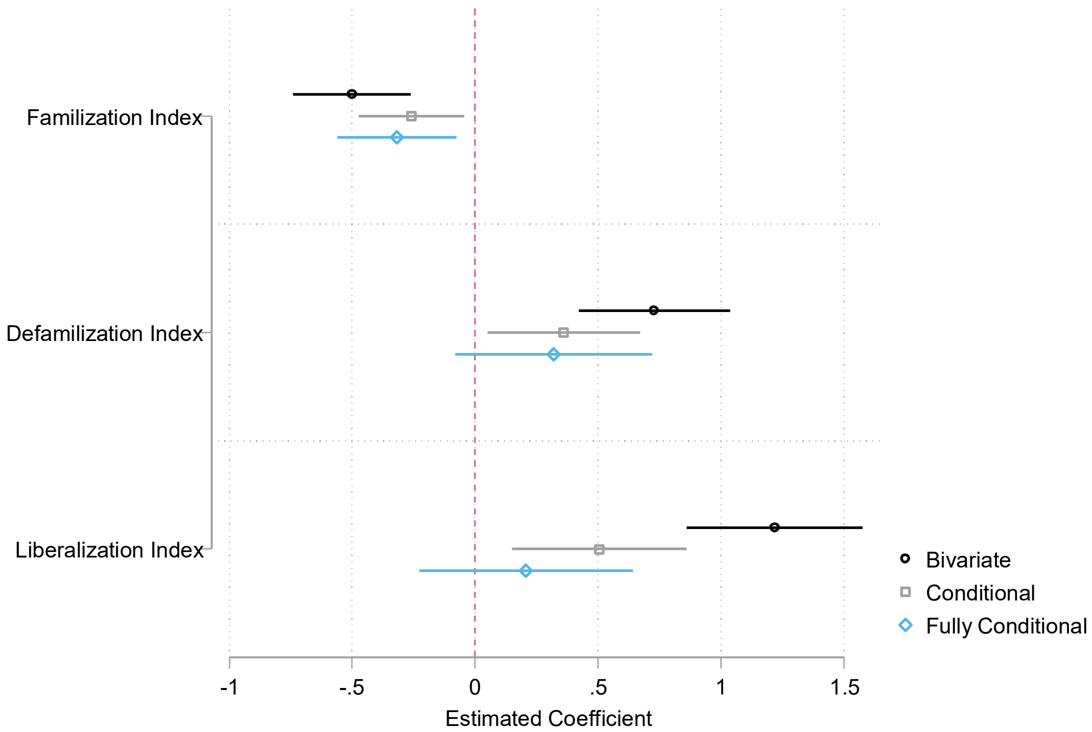




Regression Results

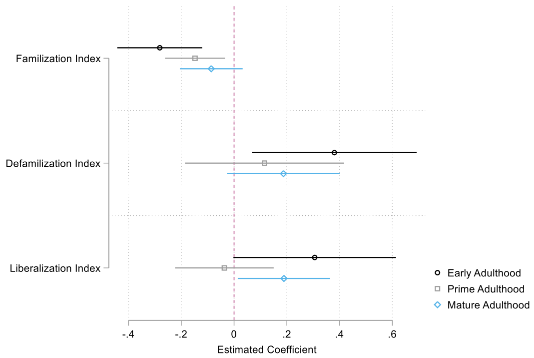
The estimated life-long familizing, defamilizing, and liberalizing policy indices on sequence complexity from country and time fixed effects regressions are displayed graphically in Figure 3. All regression results are can be found in Tables A1-A4 in the manuscript appendix. As can be seen in Figure 3, all three family policy indices present statistically significant associations with sequence complexity when unadjusted for individual and country-cohort level characteristics. For example, a one-point increase in the familization index, roughly the difference between Belgium and Austria, is associated with 0.50 point drop in sequence complexity. A one-point increase in the defamilization index, close to the difference between the 1924 and 1948 Swedish birth cohorts, is associated with a 0.72 point increase in sequence complexity. Similarly, a one-point increase in the liberalization index, approximately the difference between the Czech Republic and Belgium, is associated with 1.21 more complex sequences. Moreover, the family policy indices alone account for 12.9 to 13.2 percent of the sequence complexity variation, which is considerable for sequence based metrics (Van Winkle 2018; Van Winkle & Fasang 2017).

Figure 2: Estimated Life-long Familizing, Defamilizing, and Liberalizing Policy Index Coefficients on Sequence Complexity from Country and Time Fixed Effects Regressions



The associations between the policy indices and sequence complexity remain statistically significant when adjusted for individual and country-cohort level characteristics. However, the positive associations between defamilization and liberalization with sequence complexity are no longer statistically significant when all family policy dimensions are simultaneously estimated. Nonetheless, a one-point increase in the familization index is associated with a 0.31 point decrease in sequence complexity, even when adjusted for individual and country-cohort characteristics as well as defamilizing and liberalizing policies. These results support hypothesis H1 that familizing policies are associated with less complex family life courses. However, my results only partially support hypotheses H2 and H3 that defamilizing and liberalizing policies are associated with more complex family trajectories.

Figure 3: Estimated Early, Prime, and Mature Adulthood Familizing, Defamilizing, and Liberalizing Policy Index Coefficients on Sequence Complexity from Country and Time Fixed Effects Regressions



The fully adjusted associations between the early, prime, and mature adulthood policy indices and sequence complexity are displayed in Figure 4. As can be seen in Figure 4, the early adulthood familizing and defamilizing policy indices demonstrate statistically significant associations with sequence complexity. A one-point increase in the early adulthood familization index is associated with a 0.28 reduction in sequence complexity. An increase of one point in the early adulthood defamilization index is related with 0.38 more complex sequences. While the prime adulthood familization index is still associated with sequence complexity, the prime adulthood defamilization index is no longer significantly associated with complexity. Interestingly, the mature adulthood liberalization index displays a statistically significant association with sequence complexity. A one-point increase in the mature adulthood liberalization index is associated with 0.18 more complex sequences. Apart from liberalizing policies, the results support my hypothesis H4 that the early adulthood experience of family policies will have a greater influence on the complexity of family life courses than prime or mature adulthood experiences.

The results from country and time fixed effects regressions separately for men and women are generally consistent with those presented above (see Table A5 in the appendix). The bivariate relationships between the policy indices and sequence complexity are statistically significant for both men and women. However, the timing of family policies becomes more important in the fully adjusted models. Defamilization in early adulthood significantly increases men's sequence complexity, but only defamilization in mature adulthood increases the complexity of women's sequences. An explanation could be that high levels of defamilization after age 40 may increase the likelihood that working women enter parenthood late. It could also substantially decrease the costs of women of divorce with small children. The reverse applies for liberalizing policies: in mature adulthood they increase men's complexity, while in early adulthood increasing women's complexity. A possible explanation is that liberal abortion and divorce legislation early in life reduces the risk of pregnancy and unwanted marriage, enabling women to remain single or cohabit rather than marry. For men, liberal divorce policy in later life may simply facilitate divorce. Men and women are similar in one respect: familization in early life decreases the complexity of family sequences.

Discussion

In this study, I addressed two research questions: 1) what is the association between family policies and family life course complexity and 2) does the timing of family policies within the life course moderate this association? I hypothesized that familizing policies are associated with less complex family trajectories, while defamilizing and liberalizing policies are associated with more complex family life courses. Further, I hypothesized that familization, defamilization, and liberalization during early adulthood will be more influential than policy experiences in prime and mature adulthood. My results support my expectations to a large extent. I find that defamilization in early adulthood and liberalization in mature adulthood increase women's family life course complexity, while defamilization during mature adulthood and liberalization during early adulthood increase men's complexity. For both men and women, familization during early and prime adulthood decreases the complexity of family life courses.

My findings correspond with common accounts from the comparative family policy literature as well as family and life course sociology. Familization decreases the complexity of family life courses likely by increasing the benefits of early marriage as well as parenthood within marriage (Saraceno 2016). Direct and indirect transfers, e.g. family allowances and tax benefits, incentivize and enable a traditional male-breadwinner female-homemaker division of labor independent of economic constraints (Leitner 2003; Gauthier 2007). Therefore, women remain dependent on men's income and men remain dependent on women's care work, which increases the costs of non-marital parenthood and divorce.

At first, the results seem to indicate that familizing policies "top" defamilizing and liberalizing policies. However, a closer look reveals that it is essential to take a life course perspective when analyzing the influence of family policy on life courses (Elder et al. 2003; Dannefer 2003). Defamilization during early adulthood increases life course complexity for women, likely by increasing women's independence from the family and the opportunity costs of marriage and parenthood (Becker 1981; Becker & Tomes 1994; Esping-Andersen 1999; Lister 1994). The influence of liberalizing policies during mature adulthood on men's family life courses suggest liberal divorce legislation may decrease the attractiveness of marriage compared to other living arrangements for married men (Becker et al. 1977). However, the influence of liberalizing policies early in adulthood for women indicate that liberal divorce laws may reduce women's perceived commitment of marriage (Alesina & Giuliano 2006).

This study is not without its limitations. Despite the relatively large number of countries and wide range of birth cohorts, I cannot observe the defamilizing policies that many continental and southern European countries have implemented in the last decades (see Lohmann & Zagel 2016; Saraceno 2016; Cho 2014). For example, Germany has extensively expanded its public childcare system and is implementing a right to public childcare. Further, the comparable policy data available for my wide cohort range is limited. Although I used the best data available, policy scholars should attempt to make high quality historic information on other family related policies, such as gendered tax schemes, available to the international research community. To untangle the causal mechanisms behind the relationship between family policies and family life course complexity, future research should concentrate on small-N case studies (Mayer 2004). Countries should be chosen in a manner that allows all three policy dimensions to be simultaneously studied, because they can undermine and possibly reinforce each other.

I contribute both conceptually and empirically to the family policy and family sociological literature. First, I collect annual policy information from 1924-2008 for 15 European countries to create familization, defamilization and liberalization indices. This adds a unique historic dataset to the existing data landscape that can be used in a wide variety of research applications. Second, I use cohort rather than period policy measures or broad welfare state typologies in my analyses. Cohort measures are more nuanced policy indicators, because they express how individuals experience policies over longer segments of their life course rather than at a single age or time point. Third, I go beyond relating social policies to sequence groups and introduce sequence based metrics to the literature on social policy and life course outcomes. This methodological approach, jointly analyzing cohort policy indicators and sequence based metrics, is applicable in multiple research areas, such as labor market policy and careers (e.g. Van Winkle & Fasang 2017) or health care policy and treatment trajectories.

Finally, I demonstrate that familizing, defamilizing, and liberalizing policies are related to the complexity of family trajectories, but life course timing moderates those associations. The question of whether increasing complexity across Europe is a positive development, associated with increasing freedom of choice, or a negative trend, signaling higher volatility across the life course, was not the subject of this chapter (see chapter 6 for a discussion). However, my results indicate that a shift from familization to defamilzation along with the liberalization of family policy may have played a role in increasing family life course complexity across Europe. It is important to gain a better understanding of the long-term implications that policy shifts have for life course complexity. If the "Scandinavization" of European family policy inadvertently has negative effects on individuals' wellbeing by means of increasing uncertainty, new social policies may need to be developed to buffer those adverse effects.

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Appendix

Table A1: Country and Time Fixed Effects Regression Results of Life-Long Familization, Defamilization, and Liberalization on Sequence Complexity

	(1)	(2)	(3)	(4)	(5)	(6)	(7)
Familization	-0.501***			-0.260*			-0.319**
	(0.122)			(0.110)			(0.123)
Defamilization		0.729***			0.360*		0.320
		(0.157)			(0.158)		(0.204)
Liberalization			1.217***			0.503**	0.207
			(0.182)			(0.181)	(0.222)
Controls				✓	✓	✓	✓
N	24,234	24,234	24,234	24,234	24,234	24,234	24,234
Adj. R^2	0.129	0.130	0.132	0.163	0.163	0.163	0.164

Note: Sig.: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$; Unstandardized coefficients and standard errors in parentheses displayed. Data weighted

Table A2: Country and Time Fixed Effects Regression Results of Early Adulthood Familization, Defamilization, and Liberalization on Sequence Complexity

	(1)	(2)	(3)	(4)	(5)	(6)	(7)
Familization	-0.481***			-0.038			-0.282***
	(0.062)			(0.069)			(0.082)
Defamilization		0.392**			0.299*		0.380*
		(0.151)			(0.121)		(0.159)
Liberalization			0.675***			0.357*	0.306
			(0.152)			(0.140)	(0.157)
Controls				✓	✓	✓	✓
N	24,234	24,234	24,234	24,234	24,234	24,234	24,234
Adj. R^2	0.132	0.129	0.130	0.163	0.163	0.163	0.164

Note: Sig.: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$; Unstandardized coefficients and standard errors in parentheses displayed. Data weighted

Table A3: Country and Time Fixed Effects Regression Results of Prime Adulthood Familization, Defamilization, and Liberalization on Sequence Complexity

	(1)	(2)	(3)	(4)	(5)	(6)	(7)
Familization	-0.104			-0.143*			-0.148*
	(0.066)			(0.057)			(0.058)
Defamilization		0.330*			0.068		0.116
		(0.141)			(0.130)		(0.153)
Liberalization			0.346***			-0.002	-0.037
			(0.087)			(0.082)	(0.095)
Controls				✓	✓	✓	✓
N	24,234	24,234	24,234	24,234	24,234	24,234	24,234
Adj. R^2	0.128	0.129	0.129	0.163	0.163	0.163	0.163

Note: Sig.: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$; Unstandardized coefficients and standard errors in parentheses displayed. Data weighted

Table A4: Country and Time Fixed Effects Regression Results of Mature Adulthood Familization, Defamilization, and Liberalization on Sequence Complexity

	(1)	(2)	(3)	(4)	(5)	(6)	(7)
Familization	0.323***			-0.048			-0.087
	(0.057)			(0.059)			(0.061)
Defamilization		0.522***			0.245*		0.187
		(0.096)			(0.103)		(0.109)
Liberalization			0.421***			0.274**	0.189*
			(0.111)			(0.093)	(0.089)
Controls				✓	✓	✓	✓
N	24,234	24,234	24,234	24,234	24,234	24,234	24,234
Adj. R^2	0.130	0.131	0.129	0.163	0.163	0.163	0.164

Note: Sig.: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$; Unstandardized coefficients and standard errors in parentheses displayed. Data weighted

Table A5: Gender Specific Country and Time Fixed Effects Regression Results of Mature Adulthood Familization, Defamilization, and Liberalization on Sequence Complexity

	Men				Women			
	Long	Early	Prime	Mature	Long	Early	Prime	Mature
Familization	-0.467**	-0.378**	-0.175*	-0.076	-0.184	-0.232*	-0.112	-0.064
	(0.179)	(0.122)	(0.082)	(0.080)	(0.138)	(0.096)	(0.066)	(0.084)
Defamilization	0.203	0.503*	-0.032	-0.084	0.339	0.259	0.196	0.357**
	(0.270)	(0.208)	(0.187)	(0.154)	(0.246)	(0.192)	(0.179)	(0.136)
Liberalization	0.098	0.060	-0.071	0.378**	0.330	0.465*	0.004	0.060
	(0.319)	(0.213)	(0.127)	(0.137)	(0.271)	(0.208)	(0.126)	(0.129)
Controls	✓	✓	✓	✓	✓	✓	✓	✓
N	10,922	10,922	10,922	10,922	13,312	13,312	13,312	13,312
Adj. R^2	0.149	0.149	0.148	0.149	0.173	0.173	0.173	0.173

Note: Sig.: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$; Unstandardized coefficients and standard errors in parentheses displayed. Data weighted

CHAPTER 4

Parental Resources and the Complexity of Early Family Life Courses in the United States

Why have family life courses become more complex in the United States? According to the narrative of the Second Demographic Transition, more complex family formation is attributed to young adults from advantaged backgrounds who delay marriage and parenthood. However, the literature on social class and the transition to adulthood highlights the relationship between socio-economic disadvantage and non-marital parenthood as well as cohabitation. I incorporate metrics developed in sequence analysis in regression models to estimate the associations between parental resources and the complexity of family life courses. Using the 1979 and 1997 National Longitudinal Surveys of Youth, I construct the family life courses of men and women from age 18 to 30, born between 1961-1964 and 1980-1984 as sequences. I find no evidence that parental resources are associated with the complexity of family trajectories for men and women born between 1961-1964. For individuals born between 1980-1984, I find that living with a single parent, low parental household income, and low parental education are associated with more complex family life courses in bivariate models. However, only the association between childhood family structure and family life course complexity remains statistically significant in models adjusted for respondent's educational attainment. Contrary to the Second Demographic Transition thesis, the increasing complexity of family life courses in the United States is attributable to young adults from disadvantaged socio-economic backgrounds.

Introduction

The United States has undergone great changes since the mid-20th century, including an unprecedented increase in the diversity of family forms (Cherlin 2010) as well as a rapid rise in inequality (Heathcote et al. 2010). Within this context, the transition to adulthood has become more protracted, complex, and uncertain (Billari & Liefbroer 2010). In this study, I investigate whether the differentiation of family life courses is attributable to the pathways of young adults from advantaged or disadvantaged backgrounds. Specifically, I address two research questions: 1) what is the association between parental resources and early family life course complexity and 2) has the association between parental resources and complexity changed across birth cohorts.

In this chapter, I test four hypotheses derived from the Second Demographic Transition (SDT) thesis (Van de Kaa 1987) and the economic uncertainty framework developed by Mills & Blossfeld (2003; 2005; 2013): First, I expect that *high parental resources are associated with more complex family trajectories (H1.1)*, because socio-economically advantaged and highly educated have more liberal attitudes towards alternative family formation and are expected to be the forerunners of the SDT in society (Lesthaeghe & Surkyn 1988). Second, as postmaterialist values disseminate to all social strata, young adults from disadvantaged backgrounds may also form cohabiting unions, delay marriage and parenthood, and dissolve marital unions. Therefore, I anticipate that *the positive association between parental resources and the complexity of family trajectories is weaker for younger birth cohorts compared to older birth cohorts (H1.2).* Third and contrary to the previous two, increasing economic uncertainty during the transition to adulthood is thought to be linked with postponed marriage and parenthood as well as cohabitation and divorce (Mills & Blossfeld 2003; 2005). This means that *low parental resources are associated with more complex family trajectories (H2.1)*. As economic uncertainty rises, parents may need to assist and invest more in their children to prevent downward social mobility (Breen & Goldthorpe 1997; Bernardi & Grätz 2015). Above traditional parental resources, McLanahan's (2004) diverging destinies hypothesis maintains childhood family structure is increasingly important for children's family outcomes. Therefore, *the negative association between parental resources and the complexity of family trajectories is stronger for younger birth cohorts compared to older birth cohorts (H2.2)*.

Data & Methods

Study Sample & Sequence Definition

I prepared the NLSY79[21] and the NLSY97[22] to study the association between parental resources and the complexity of children's family trajectories. The main NLSY79 sample consists of 12,686 respondents born between 1957 and 1964 that were first interviewed in 1979. Of those, 5,945 were observed at age 18, i.e. born between 1961 and 1964.The NLSY97 sample consists of 8,948 respondents born between 1980 and 1984 that were first interviewed in 1997. Both panel studies continued to collect economic, sociological and demographic information annually, biannually since 1994 for the NLSY79 and 2011 for the NLSY97. I use prospective and retrospective data to construct family sequences with monthly information from age 18 to 30. Sequences consist of 156 consecutive states, which can be in the parental home (P), living outside the parental home and not with a partner (S), living with an unmarried partner (C), in marriage (M) or divorced (D). All states can be further differentiated for having 1, 2, or 3 or more children (e.g. M1C, M2C, M3C). Note that the results presented below are robust to more differentiated sequence alphabets, e.g. for higher parity births and higher order marriages.

Residential information is collected annually in both the NLSY79 and NLSY97 studies. While the NLSY79 study reports the household type of the respondent, the NLSY97 collects information on all members living in a respondent's household and their relationship to the respondent. I consider NLSY97 respondents to be living in the parental home if a biological, step or adoptive parent is living in the same household. Information on living independently, in cohabitation and in marriage as well as fertility information is prepared as monthly variables in the NLSY97. However only marriage and fertility information is prepared in the NLSY79. Cohabitation spells were collected retrospectively starting in 1990 if cohabitation preceded the current marriage or when cohabitation with the respondent's current partner began. This could lead to an underestimation of cohabitation spells for the NLSY79 cohort. I consider NLSY79 respondents to be single, i.e. living in an independent household, if they are neither living in the parental household, cohabiting, nor married. I retain 4,798 sequences from the NLSY79

[21] The NLSY79 survey is sponsored and directed by the U.S. Bureau of Labor Statistics and conducted by the Center for Human Resource Research at The Ohio State University. Interviews are conducted by the National Opinion Research Center at the University of Chicago

[22] The NLSY97 survey is sponsored and directed by the U.S. Bureau of Labor Statistics and conducted by the National Opinion Research Center at the University of Chicago, with assistance from the Center for Human Resource Research at The Ohio State University.

study born between 1961 and 1964, and 5,836 sequences from the NLSY97 study born between 1980 and 1984.

Measuring Parental Resources

I measure parental resources using parental education, relative equivalized household income, and childhood family structure. Parental education is the average of respondents' biological mother's and father's education in years[23]. If information on mother's or father's education is missing, e.g. in single parent households, then the education of the parent present is used. This variable is constructed using information reported by the respondent in 1979 and 1997 for the NLSY79 and the NLSY97, respectively.

The ability of parents to support their children financially is measured as the relative equivalized net household income averaged over the years that the respondent was between age 18 and 21.[24] Household income values are averaged for two reasons: First, financial support between these ages is extremely important for a smooth transition to adulthood. During this period, young adults are visiting and entering higher education institutions, leaving the parental home, and entering the labor market. Second, parental household income is only measured when respondents are living with their parents. Therefore, the proportion of missing values is high if only a single year, e.g. at age 18, is taken.

Relative income, i.e. the position of the parental household in the household income distribution, should be used rather than absolute income to ensure comparability across study cohorts for two reasons: First, it is important to use an income measure that accounts for changed consumption aspirations across social strata and birth cohorts as well as the social and economic constraints to achieve these aspirations (Crimmins et al. 1991). Second, relative income increases the comparability between the types of income collected in the two studies. Gross household income is collected in the NLSY97 including the incomes of all household members over age 14. Net household income for all household members related to the respondent is collected in the NLSY79. The household incomes for both the NLSY97 and the NLSY79 include government transfers, e.g. social assistance. For the NLSY97, I approximate net income by estimating the marginal income tax for the given year and subtract the respective

[23] Substantively similar results are retrieved with regressions conducted with a categorical measure of parental and respondents' educational attainment (less than high school, completed high school, and more than high school).
[24] Note that income is reported for the previous year, i.e. ages 17-20.

sum from gross income. I adjust yearly incomes for inflation, calculate income means, and finally the percentiles of these means within each study cohort, which are reported as income deciles in the analyses below.

I additionally include an indicator for childhood family structure in the analysis. This indicator is binary and indicates whether respondents lived with both biological parents or not at age 14 for the NLSY79 and at age 12 for the NLSY97. Respondents who were not living with both biological parents were most commonly living in single mother households, although some reported single father households, step-family or other more complex arrangements. Although a more nuanced family structure indicator would be better, small sample sizes make a further differentiation impracticable. My binary indicator nonetheless accounts for differences between two-parent families and other family forms beyond education and income, such as the socialization of family related values and norm, ability to supervise and control children's activities, and stress due to household instability (see Teachman 2003 for an overview).

Analytical Strategy

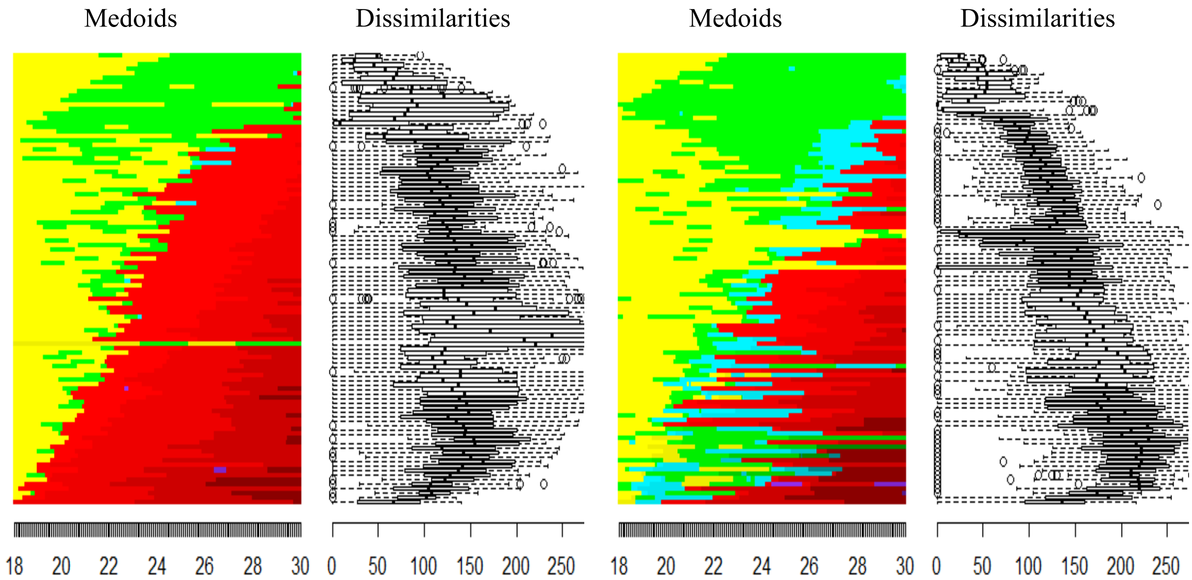
The relationships between my indicators for parental resources and sequences complexity are estimated using linear regressions. I estimate each parental resource separately (model 1), in a joint model (model 2), and in a model additionally adjusted for educational attainment (model 3). Models are estimated separately by gender and race to uncover any differences in effect sizes that may otherwise be masked in a combined sample. All models are adjusted for respondents' year of birth. As a sensitivity test, I included parental and respondents' educational attainment as a categorical variable (less than high school, high school, more than high school). The results of these analyses are substantively similar to those presented below. To account for a high level of missing information, especially childhood family structure and parental household income, I used multiple imputation with chained equations.[25] The results are largely robust to analyses using non-imputed data and lead to the same substantive conclusions. I use the sampling panel weight provided by the NLSY studies for the wave when the respondent turned 30, i.e. the last observation used to construct the analysis sample. These weights are used throughout all analysis steps and correct for oversampling and selective panel attrition.

[25] I include all model covariates as well as biannual sequence states in the imputation models. Twenty imputed datasets are generated, each with 100 burn-in iterations.

Results

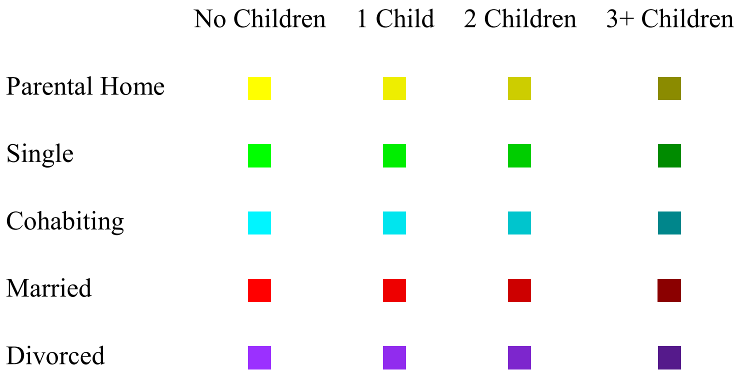
Descriptive Results

Figure 1: Relative Frequency Sequence Plots by Study Cohort



Representation Quality: $R^2 = 0.31$ and F = 21.18 Representation Quality: $R^2 = 0.27$ and F = 21.29

Legend



The family sequences of the NLSY79 and NLSY97 respondents are displayed as relative frequency sequence plots (Fasang & Liao 2014) in Figure 1.[26] Individual medoid sequences are

[26] Relative frequency sequence index plots are generated in 4 steps: 1) sorting sequences using a sorting criteria, 2) dividing the sample subgroups, 3) choosing one medoid sequence per subgroup as a representative, and 4) plotting the medoid sequences according to the sorting criteria in step 1.[26] I use divide the sample into 100 subgroups and the first factor derived from multidimensional scaling as a sorting criterium. The plots were created

displayed on the left and dissimilarities to those sequences are displayed as box plots on the right separately for the NLSY79 and NLSY97 cohorts. These plots clearly demonstrate that individuals born 1980-1984 are less likely to enter marriage and parenthood before age 30 than those born 1961-1964. As can be seen in the medoid plot on the far left, men and women born in the early 1960s married and entered parenthood shortly after leaving the parental home in their early 20s. The family life courses of young adults born in the early 1980s often lived independently or cohabited after leaving the parental home before entering marriage in their late 20s. Although members of the NLSY97 study cohort left the parental home somewhat later than members of the NLSY79 cohort, returning to the parental home was not uncommon for either cohort. In sum, the relative frequency sequence plots give the impression that the early family life courses of the younger cohort are characterized by more transitions and more unpredictability than the older cohort.

Indeed, as can be seen in Table 2, the complexity of family life courses has increased from an average 9.6 for the NLSY79 cohort to 10.4 for the NLSY97 cohort. Summary statistics of the non-imputed sample are displayed in Table 2 by study cohort. The variation of sequence complexity has also increased across cohorts, which reflects the increase in foregoing marriage and parenthood before age 30 as well as the increase in cohabitation preceding marriage. As expected, parental household income and parental education has increased across the two cohorts. While young adults born between 1961-1964 lived in parental households with an average equivalized income of 36,000 dollars, this increased to nearly 45,000 for young adults born between 1980-1984. Further, average parental education was under 12 years for the older birth cohort, while parents had an average of 13 years for the younger cohort. Similarly, respondents' average educational attainment increased from 13.5 to 14.5 years across the two cohorts. The share of young adults that reported living outside a household with two biological parents increased from 27 % to 41 % across the NLSY study cohorts.

Results from Regression Analysis

The estimated associations between relative parental household income, parental education, childhood family structure, and educational attainment with sequence complexity are displayed by study, gender, and race in Figure 2. The results for the NLSY79 cohort are displayed on the left of each panel and the NLSY97 cohort results are presented on the right. The three graphs

with the the seqplot.rf function developed by Matthias Studer, Anette Fasang and Tim Liao implemented in the TraMineRextras package using R.

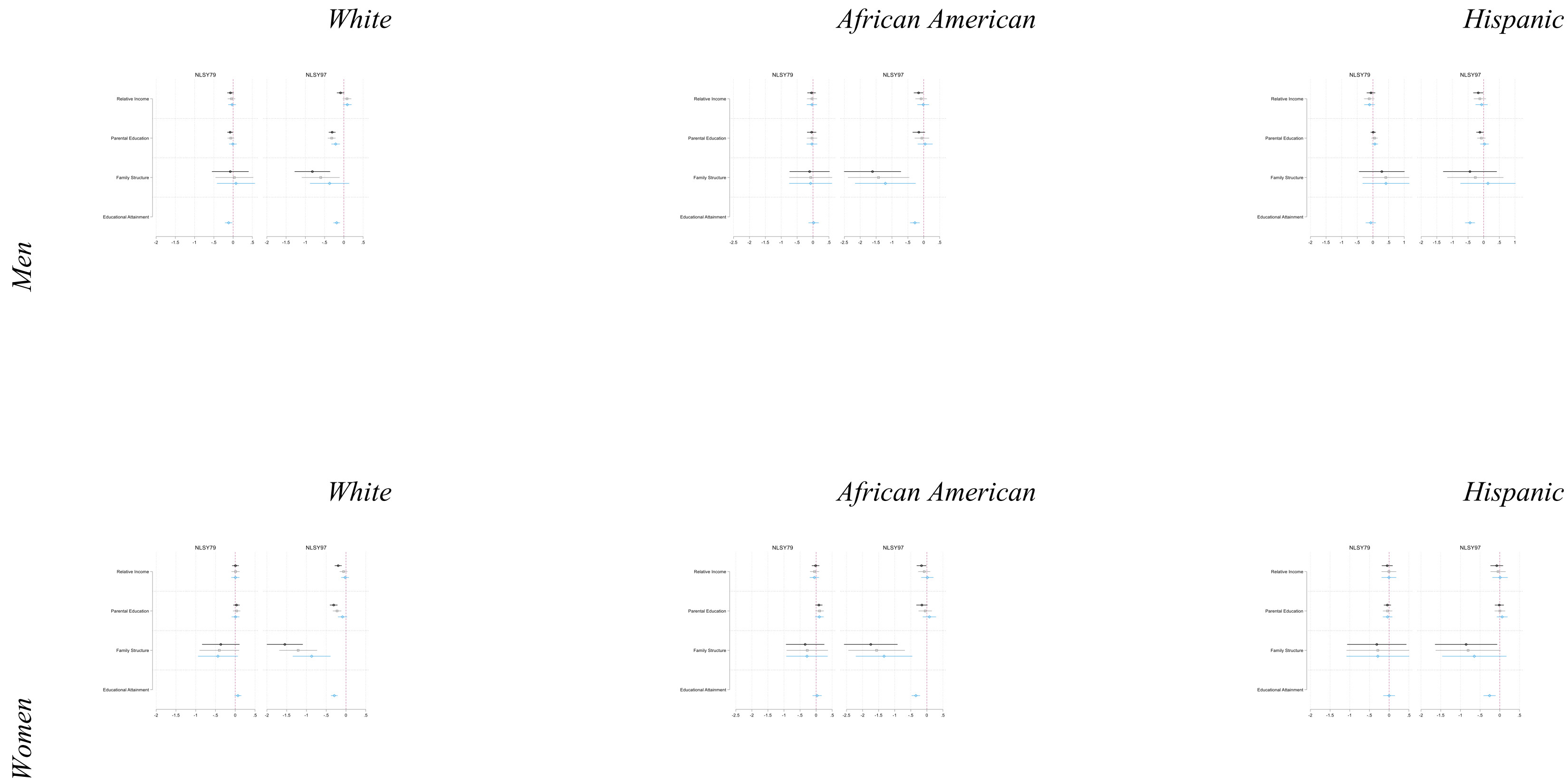
in the first row show the coefficients for white, African American, and Hispanic men (from left to right). The results for women are displayed in the second row. The regression results are additionally displayed in Tables A1-A6 in the manuscript appendix. An additional table is included in the appendix displaying regression results for the entire sample adjusted for gender and race (see Table A7).

Table 1: Summary Statistics of the NLSY79 & NLSY97 Sample

	NLSY79	NLSY97
Complexity	9.65	10.48
	(3.44)	(4.38)
Eq. Parental HH Income	36,023.50	44,878.13
	(21,172.85)	(32,249.53)
Parental Education	11.59	13.09
	(2.79)	(2.68)
Childhood Family Structure		
Two Parent	0.73	0.59
	(0.44)	(0.49)
Other	0.27	0.41
	(0.44)	(0.49)
Educational Attainment	13.51	14.54
	(2.46)	(3.01)
Gender		
Men	0.52	0.55
	(0.50)	(0.50)
Women	0.48	0.45
	(0.50)	(0.50)
Race		
Hispanic	0.06	0.13
	(0.24)	(0.34)
African American	0.13	0.15
	(0.33)	(0.36)
White	0.81	0.71
	(0.39)	(0.45)
N	3,940	3,856

Note: Means or proportions and standard deviations in parentheses displayed; Data weighted.

Figure 2: Estimated Regression Coefficients on Sequence Complexity by Study, Gender, and Race



As can be seen on the left of each panel, there are no substantially significant associations between any covariates and sequence complexity for members of the NLSY79 study cohort. I only find statistically significant negative associations for white men. Parental education is negatively associated with sequence complexity in the bivariate NLSY79 model, but is no longer statistically different from zero in models adjusted for parental household income, childhood family structure, or respondents' education. However, a one-year increase in white men's education is associated with a 0.12 decrease in complexity. Substantively, this is a relatively weak association: a one standard deviation increase in educational attainment is only associated with a 0.09 standard deviation increase in sequence complexity.

There is a general negative tendency for the bivariate associations between parental income, parental education, and childhood family structure, and sequence complexity for the NLSY97 cohort. However, the substantial and statistical significance of these associations vary greatly by gender and race. Relative parental household income is statistically significant for all subpopulations, except for Hispanic women. The strongest effect can be found among white women, where a one decile increase in parental household income is associated with 0.2 more complex family sequences. Higher levels of parental education are associated with less complex family sequences, particularly for white men and women. For white women, an increase in one year of parental education is related with a 0.31 increase in complexity. Aside from Hispanic men, living with both biological parents during childhood and adolescence is associated with a decrease in sequence complexity. Childhood family structure is especially relevant for African American women, where living in a two-parent household is associated with 1.74 more complex sequences, well over a one-third of a standard deviation.

When parental income, parental education, and childhood family structure are estimated in a joint model, there are no longer any statistically significant associations between income and sequence complexity. However, the statistically significant association between parental education and complexity remains for white men and women. Interestingly, the relationship between parental education and complexity diminishes slightly for women while remaining unchanged for men. Family structure also remains significantly associated with sequence complexity for African American and white men and women. Although the associations are slightly weaker, they still range from approximately one-fifth to one-third of a standard deviation of complexity.

Many of these associations are substantially attenuated when respondent's educational attainment is included in the models, which indicates that the relationship between parental resources and complexity is partially mediated by educational attainment. This is in line with arguments that children with higher parental incomes and education as well as children growing up with two parents are more likely to attain a higher educational level and delay marriage and parenthood. Parental education is significantly related with complexity only for white men, where an increase in one year of parental education is associated with a 0.21 decrease in complexity. Childhood family structure remains statistically associated with sequence complexity for white women as well as for African American men and women. The largest relationship is still for African American women, where the association is over one-fourth of a standard deviation of sequence complexity.

Educational attainment is the only factor with a statistically and often substantively significant association with the complexity of family sequences across all subgroups. The weakest relationship with education is found among white men: an increase in 1 year of education is associated with only a 0.19 decrease in complexity. The association is strongest among Hispanic men: a one-year increase in education relates to a 0.44 decrease in complexity. In other terms, a one standard deviation change in education for Hispanic men is associated with nearly a quarter standard deviation change in sequence complexity.

Discussion

In this study, I have attempted to add to the previous descriptive literature on family life course complexity by investigating individual factors that might be associated with complexity. Specifically, I sought to ascertain 1) whether parental resources are associated with early family life course complexity and 2) whether the association between parental resources and complexity changed across birth cohorts. On the one hand, I drew on the classical narrative of the SDT thesis to generate hypotheses that higher parental resources are associated with more complex family life courses and that this association would weaken across birth cohorts (H1.1 & H1.2). On the other hand, I used current research on the association between economic change, social class, and the transition to adults to hypothesize that higher parental resources are associated with less complexity, but that this association would grow stronger across cohorts (H2.1 & H2.2). Results using data from the NLSY79 and NLSY97 support hypotheses H2.1 and H2.2: Although parental resources are negatively associated with the complexity of family life courses of individuals born between 1981-1984, there are no substantively or statistically significant associations for individuals born between 1961-1964.

I find limited support for the relationship between parental resources and family life course complexity posited by the SDT thesis. Socio-economically advantaged and highly educated individuals are expected to be the forerunners of the SDT with lower rates of marriage and parenthood along with higher rates of cohabitation and divorce (Van de Kaa 1987; Lesthaeghe & Johan Surkyn 1988). However, I find no evidence that high parental resources are associated with more complex family formation trajectories. Further, I find no evidence that the association between parental background and complexity has weakened, which would have indicated a dissemination of family demographic behavior associated with the SDT across broader segments of society.

Rather, my results support one of the main competitors of the SDT: Mills & Blossfeld's (2003; 2005; 2013) globalization and economic uncertainty framework. My results for white men support the argument that less educated parents may find it more difficult to support their children during the college application process through to graduation (Lareau 2011b; 2011a), diminishing their chances for stable and gainful employment (Kalleberg 2009). In a precarious labor market position, these young men may find it difficult to enter marriage and parenthood (Oppenheimer 1988; Oppenheimer & Kalmijn 1995; Easterlin 1975; 1976) and turn to cohabiting unions instead (Oppenheimer 2003). The association between parental education and life course complexity has also grown stronger for white men across birth cohorts, which may indicate that highly educated parents are investing more in their children in nonfinancial ways.

Childhood family structure is the most influential parental background characteristic associated with family life course complexity. Young adults who grew up with both biological parents in their childhood household have less complex family life courses. Moreover, the association between family structure and complexity has grown stronger across birth cohorts even when adjusted for parental education and income. This supports McLanahan's (2004) diverging destinies hypothesis and adds evidence that childhood family structure is related to young adults' family demographic behavior above and beyond selection mechanisms (Ryan et al. 2009; Raab 2017). One possible mechanism could lie in the transmission of family values, norms, and preferences, which can manifest itself in the intergenerational transmission of fertility (Fasang 2015), cohabitation (Teachman 2003), marriage and divorce (Amato & DeBoer 2001; Wolfinger 2011), or even holistic family trajectories (Fasang & Raab 2014). Other mechanisms could include family instability and higher stress levels that may induce early union formation and parenthood (Fomby & Bosick 2013).

I also demonstrate that educational attainment is strongly associated with family life course complexity for younger birth cohorts. Higher educational attainment is related with less complex family trajectories, likely consisting of living in the parental home or in an independent household followed by delayed marriage and parenthood. Moreover, a substantial portion of the effects of parental income, parental education, and childhood family structure on life course complexity runs through young adults' educational attainment. This is in line with arguments that parents invest and in their children's education (Breen & Goldthorpe 1997) and that parents with high resources will compensate for their children's disadvantages to ensure their success (Erola & Kilpi-Jakonen 2017; Bernardi & Grätz 2015). It also indicates that the association between family structure and complexity is partially attributed to two-parent families' greater capacity for social control, e.g. supervising the completion of high school (Astone & McLanahan 1991; Thomson et al. 1992).

There are of course challenges to this study, one of which is the short duration of the family formation process that I can observe. I likely miss entry into co-residential unions and parenthood for many highly educated respondents, especially for the 1980-1984 birth cohort. And while I observe several divorces, I likely do not observe other union dissolutions and subsequent remarriages, and childbirth within higher order marriages that are more common among adults from disadvantaged socio-economic backgrounds. My estimate of complexity levels and the estimated associations between parental resources and family formation complexity are likely conservative, because I cannot yet observe these increasingly complex family formation process. As longitudinal studies, such as the NLSY79 and the NLSY97, continue to mature, the association between parental resources and the complexity of family formation in the United States should be revisited.

While some scholars optimistically argue that complexity is the result of increasing individual freedom from social institutions (Beck 1994; 2009), my results indicate that family life course differentiation is the consequence of an increasingly volatile transition to adulthood (see chapter 6 for a discussion on the subjective meaning of complexity for individuals). It is important to understand the relationship between parental resources and family formation differentiation, because complex family pathways involving early parenthood outside of marriage and early union formation are also those with the highest poverty risk (Mclanahan 2011; McLanahan & Percheski 2008). Without adequate social institutions to provide disadvantaged young adults access to higher education and a smooth transition into the labor market, the relationship between disadvantaged socio-economic background and disadvantaged family formation may become increasingly self-reinforcing. To this end, future research needs to concentrate on whether low parental household income and parental education is associated with more complex family formation trajectories in other contexts where young adults are less reliant on parental resources due to social welfare institutions.

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Appendix

Table A1: Regression Results of Parental Resources on Family Sequence Complexity for the Entire Sample

	1		2		3		4		5	
	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97
Eq. Parental HH Income	-0.03	-0.15^{***}					-0.02	-0.02	-0.02	0.01
	(0.02)	(0.03)					(0.03)	(0.03)	(0.03)	(0.03)
Parental Education			-0.02	-0.23^{***}			-0.00	-0.19^{***}	0.00	-0.08^{*}
			(0.02)	(0.03)			(0.03)	(0.03)	(0.03)	(0.03)
Family Structure (ref.: 2 Parents)										
Other					-0.21	-1.16^{***}	-0.18	-0.96^{***}	-0.17	-0.65^{***}
					(0.14)	(0.13)	(0.14)	(0.14)	(0.14)	(0.14)
Educational Attainment									-0.02	-0.28^{***}
									(0.03)	(0.02)
Gender (ref.: Men)										
Women	-0.06	1.06^{***}	-0.06	1.09^{***}	-0.06	1.06^{***}	-0.06	1.05^{***}	-0.05	1.28^{***}
	(0.12)	(0.13)	(0.12)	(0.13)	(0.12)	(0.13)	(0.12)	(0.13)	(0.12)	(0.13)
Race (ref.: Hispanic)										
Black	0.22	0.60^{**}	0.29^{+}	1.07^{***}	0.21	0.35^{+}	0.21	0.70^{**}	0.20	0.63^{**}
	(0.17)	(0.20)	(0.17)	(0.21)	(0.17)	(0.21)	(0.18)	(0.22)	(0.18)	(0.21)
White	0.21	0.27	0.20	0.66^{***}	0.17	0.08	0.22	0.64^{***}	0.21	0.56^{**}
	(0.15)	(0.18)	(0.16)	(0.19)	(0.15)	(0.17)	(0.16)	(0.19)	(0.16)	(0.19)
Constant	9.39^{***}	9.57^{***}	9.36^{***}	9.16^{***}	9.55^{***}	10.30^{***}	9.50^{***}	9.76^{***}	9.50^{***}	9.55^{***}
	(0.14)	(0.17)	(0.15)	(0.18)	(0.17)	(0.18)	(0.18)	(0.20)	(0.18)	(0.19)
N	4798	5848	4798	5848	4798	5848	4798	5848	4798	5848

Note: Sig.: + p < .1, * p < .05, ** p < .01, *** p < .001; Unstandardized coefficients and standard errors in parentheses displayed; Coefficients for birth year omitted; Pooled regression results using 20 multiply imputed datasets; Data weighted.

Table A2: Regression Results of Parental Resources on Family Sequence Complexity for White Men

	1		2		3		4		5	
	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97
Eq. Parental	-0.07	-0.09^{+}					-0.04	0.08	-0.03	0.09
HH Income	(0.04)	(0.05)					(0.05)	(0.06)	(0.05)	(0.06)
Parental			-0.08*	-0.30***			-0.06	-0.31***	-0.01	-0.21***
Education			(0.04)	(0.05)			(0.04)	(0.05)	(0.05)	(0.06)
Family Structure										
(ref.: 2 Parents)										
Other					-0.07	-0.82***	0.03	-0.60*	0.07	-0.37
					(0.24)	(0.24)	(0.25)	(0.25)	(0.25)	(0.26)
Educational									-0.12*	-0.19***
Attainment									(0.05)	(0.04)
Constant	9.62***	9.67***	9.55***	9.74***	9.58***	10.07***	9.58***	10.03***	9.51***	9.83***
	(0.12)	(0.13)	(0.10)	(0.12)	(0.21)	(0.19)	(0.21)	(0.18)	(0.22)	(0.19)
N	1,368	1,488	1,368	1,488	1,368	1,488	1,368	1,488	1,368	1,488

Note: Sig.: + p < .1, * p < .05, ** p < .01, *** p < .001; Unstandardized coefficients and standard errors in parentheses displayed; Coefficients for birth year omitted; Pooled regression results using 20 multiply imputed datasets; Data weighted.

Table A3: Regression Results of Parental Resources on Family Sequence Complexity for African American Men

	1		2		3		4		5	
	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97
Eq. Parental	-0.05	-0.16*					-0.03	-0.08	-0.04	-0.02
HH Income	(0.07)	(0.08)					(0.08)	(0.09)	(0.08)	(0.09)
Parental			-0.04	-0.16			-0.03	-0.06	-0.03	0.04
Education			(0.07)	(0.10)			(0.08)	(0.12)	(0.09)	(0.12)
Family Structure										
(ref.: 2 Parents)										
Other					-0.11	-1.61***	-0.07	-1.42**	-0.08	-1.21*
					(0.32)	(0.46)	(0.34)	(0.49)	(0.34)	(0.49)
Educational									0.02	-0.28***
Attainment									(0.08)	(0.08)
Constant	9.70***	10.68***	9.73***	10.79***	9.81***	11.25***	9.73***	11.07***	9.74***	10.77***
	(0.18)	(0.23)	(0.17)	(0.21)	(0.23)	(0.23)	(0.27)	(0.28)	(0.27)	(0.28)
N	608	796	608	796	608	796	608	796	608	796

Note: Sig.: + p < .1, * p < .05, ** p < .01, *** p < .001; Unstandardized coefficients and standard errors in parentheses displayed; Coefficients for birth year omitted; Pooled regression results using 20 multiply imputed datasets; Data weighted.

Table A4: Regression Results of Parental Resources on Family Sequence Complexity for Hispanic Men

	1		2		3		4		5	
	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97
Eq. Parental	-0.06	-0.17*					-0.12	-0.12	-0.11	-0.07
HH Income	(0.07)	(0.08)					(0.08)	(0.10)	(0.09)	(0.10)
Parental			0.01	-0.12*			0.05	-0.07	0.06	0.03
Education			(0.04)	(0.06)			(0.05)	(0.07)	(0.05)	(0.07)
Family Structure										
(ref.: 2 Parents)										
Other					0.28	-0.44	0.41	-0.27	0.42	0.14
					(0.37)	(0.44)	(0.38)	(0.46)	(0.38)	(0.45)
Educational									-0.07	-0.44***
Attainment									(0.08)	(0.08)
Constant	9.62***	9.52***	9.67***	9.36***	9.47***	9.85***	9.48***	9.54***	9.46***	9.14***
	(0.18)	(0.22)	(0.21)	(0.27)	(0.29)	(0.32)	(0.32)	(0.36)	(0.32)	(0.36)
N	398	635	398	635	398	635	398	635	398	635

Note: Sig.: + p < .1, * p < .05, ** p < .01, *** p < .001; Unstandardized coefficients and standard errors in parentheses displayed; Coefficients for birth year omitted; Pooled regression results using 20 multiply imputed datasets; Data weighted.

Table A5: Regression Results of Parental Resources on Family Sequence Complexity for White Women

	1		2		3		4		5	
	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97
Eq. Parental	0.01	-0.20***					0.01	-0.06	0.00	-0.02
HH Income	(0.04)	(0.05)					(0.05)	(0.05)	(0.05)	(0.05)
Parental			0.03	-0.31***			0.03	-0.23***	0.01	-0.09
Education			(0.04)	(0.05)			(0.05)	(0.05)	(0.05)	(0.06)
Family Structure										
(ref.: 2 Parents)										
Other					-0.37	-1.55***	-0.40	-1.21***	-0.44+	-0.87***
					(0.24)	(0.23)	(0.26)	(0.24)	(0.26)	(0.24)
Educational									0.07	-0.30***
Attainment									(0.04)	(0.04)
Constant	9.52***	11.07***	9.52***	11.08***	9.81***	11.78***	9.81***	11.76***	9.84***	11.67***
	(0.12)	(0.12)	(0.10)	(0.12)	(0.21)	(0.18)	(0.21)	(0.18)	(0.21)	(0.17)
N	1,398	1,460	1,398	1,460	1,398	1,460	1,398	1,460	1,398	1,460

Note: Sig.: + p < .1, * p < .05, ** p < .01, *** p < .001; Unstandardized coefficients and standard errors in parentheses displayed; Coefficients for birth year omitted; Pooled regression results using 20 multiply imputed datasets; Data weighted.

Table A6: Regression Results of Parental Resources on Family Sequence Complexity for African American Women

	1		2		3		4		5	
	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97
Eq. Parental	-0.02	-0.17*					-0.05	-0.08	-0.05	0.02
HH Income	(0.06)	(0.08)					(0.07)	(0.09)	(0.07)	(0.10)
Parental			0.09	-0.15^{+}			0.11^{+}	-0.05	0.10	0.08
Education			(0.06)	(0.09)			(0.07)	(0.11)	(0.07)	(0.11)
Family Structure										
(ref.: 2 Parents)										
Other					-0.34	-1.74***	-0.28	-1.56***	-0.28	-1.33**
					(0.30)	(0.42)	(0.33)	(0.45)	(0.33)	(0.45)
Educational									0.03	-0.34***
Attainment									(0.07)	(0.07)
Constant	9.47***	10.59***	9.57***	10.78***	9.65***	11.25***	9.65***	11.05***	9.64***	11.19***
	(0.17)	(0.22)	(0.15)	(0.19)	(0.20)	(0.21)	(0.25)	(0.26)	(0.25)	(0.27)
N	593	840	593	840	593	840	593	840	593	840

Note: Sig.: + p < .1, * p < .05, ** p < .01, *** p < .001; Unstandardized coefficients and standard errors in parentheses displayed; Coefficients for birth year omitted; Pooled regression results using 20 multiply imputed datasets; Data weighted.

Table A7: Regression Results of Parental Resources on Family Sequence Complexity for Hispanic Women

	1		2		3		4		5	
	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97	NLSY79	NLSY97
Eq. Parental	-0.05	-0.08					-0.01	-0.04	-0.01	0.01
HH Income	(0.07)	(0.08)					(0.09)	(0.10)	(0.09)	(0.10)
Parental			-0.04	-0.01			-0.04	0.00	-0.04	0.06
Education			(0.05)	(0.06)			(0.06)	(0.07)	(0.06)	(0.07)
Family Structure										
(ref.: 2 Parents)										
Other					-0.31	-0.86*	-0.29	-0.80+	-0.29	-0.65
					(0.38)	(0.40)	(0.41)	(0.42)	(0.41)	(0.42)
Educational									-0.00	-0.26**
Attainment									(0.08)	(0.08)
Constant	9.07***	10.76***	8.95***	10.82***	9.31***	11.28***	9.16***	11.21***	9.16***	11.15***
	(0.18)	(0.23)	(0.24)	(0.26)	(0.33)	(0.29)	(0.37)	(0.34)	(0.38)	(0.34)
N	433	629	433	629	433	629	433	629	433	629

Note: Sig.: + p < .1, * p < .05, ** p < .01, *** p < .001; Unstandardized coefficients and standard errors in parentheses displayed; Coefficients for birth year omitted; Pooled regression results using 20 multiply imputed datasets; Data weighted.

CHAPTER 5

Genome-Wide Heritability Estimates for Family Life Course Complexity

Sequence analysis is an established method to study the social antecedents of life course complexity. Rather than studying a series of single indicators, sequence analysis enables scholars to investigate complexity as a holistic outcome. Both individual and societal characteristics have been linked with the complexity of individuals' family trajectories. However, life course sociologists have largely neglected the potential role of genetic factors when studying the complexity of family trajectories. I apply retrospective life history and molecular genetic data from the US Health and Retirement Study (HRS) to a genome-wide complex trait analysis (GCTA). Specifically, I estimate the genetic component of sequence complexity using genomic-relatedness-based restricted maximum-likelihood (GREML) models. This innovative methodological approach allows me to estimate the heritability of family life course complexity across several US birth cohorts for the first time. My results indicate that 10 percent of the total variation in family life course complexity is attributable to genetic influences. Further, specific aspects of family complexity, such as age at first birth and marriage, are substantially influenced by genes. I find no evidence that heritability has changed across birth cohorts in the United States. Therefore, my results do not substantiate claims that lower normative constraints on family demographic behavior increase the role of genetic predispositions. I discuss the implications of my results for further biodemographic research on family demographic behavior and life course complexity.

Introduction

Family sociologists and demographers work under the impression that family life courses have become more complex, unstable, and unpredictable (Walsh 2012). The United States has seen a decrease and postponement in marriage and fertility coinciding with an increase in nonmarital cohabitation and fertility as well as divorce and remarriage (Cherlin 2010). Three meta-theoretical narratives are commonly applied when studying family life course complexity: First, the Second Demographic Transition (SDT) thesis is an ideational account, which associates more complex family life courses with a shift from materialist to post-materialist values (Van de Kaa 1987; 2001; Lesthaeghe 1995; 2010; 2014). Second, an increase in family life courses has been connected with increasing economic uncertainty following globalization and deindustrialization (Mills & Blossfeld 2005; 2003; 2013). Third, life courses sociologists and welfare state scholars argue that labor market and family policies are related to the complexity of family lives (Esping-Andersen 1990; 1999; Mayer 1997; 2004; 2009). The first two theoretical perspectives are generally invoked to account for change over time, while the latter is more commonly used to account for cross-national differences. However, a fourth theoretical perspective on family demographic behavior is currently emerging: biodemography (Kohler et al. 2006; Mills & Tropf 2015; Conley 2016). This approach concentrates on genetic factors that influence the components of family life course complexity.

The first step in biodemographic research is the estimation of heritability. Heritability is the proportion of phenotypic or trait variance that is attributed to genetic factors as opposed to environmental factors. The strength of heritability gives researchers insight on the potential importance of sociobiological explanations and the consequences of ignoring them. Most heritability estimates for family demographic behavior have compared monozygotic and dizygotic twins (see Boomsma et al. 2002 for heritability estimation with ACE models; Kohler et al. 1999; Tropf et al. 2015a for fertility; Johnson et al. 2004 for marriage; Jocklin et al. 1996; McGue & Lykken 1992 for divorce). However, twin ACE models have strong assumptions, which lead to biased heritability estimates if violated (Horwitz et al. 2003). More precise heritability estimates can be determined using genome-wide complex trait analysis (GCTA), which utilizes genetic similarity to decompose trait variance into a genetic and an environmental component (Domingue et al. 2016; Yang et al. 2011; Yang et al. 2010). So far only Tropf and colleagues (2015b) have used genomic-relatedness-based restricted maximum-likelihood (GREML) models to estimate the heritability of fertility. There are no studies that estimate heritability using GCTA for other family demographic outcomes, such as marriage or divorce.

In this chapter, I estimate the heritability of family life course complexity, the age of first birth and first marriage, and the number of children, marriages, and divorces using GCTA with data from the US Health and Retirement Study (HRS). Based on the large heritability estimates found using twin studies, I expect *the complexity of family trajectories as well as its components will be heritable in the United States* (H1). Kohler and colleagues (2006) argue that the heritability of fertility is attributable to 1) direct biological effects, 2) indirect effects on conscious decision-making, and 3) indirect effects on subconscious decision-making. More broadly, Freese (2008) discusses how genetic factors work directly and indirectly through intermediate phenotypes (see chapter 1 for a more thorough discussion). These intermediate phenotypes, e.g. height, personality, or cognitive ability, may have direct effects on an outcome, such as the decision to marry. However, intermediate phenotypes can also affect the relationship between an outcome and its social determinants by moderating the relationship, confounding the relationship, or predetermining the social determinant. It seems plausible that genetic factors will affect family life course complexity directly, e.g. biological determinants of fertility, and indirectly through intermediate phenotypes and the social antecedences of complexity, some of which were discussed in chapter 4.

Institutional and other environmental conditions, such as those discussed in chapters 2 and 3, may affect the relationship between intermediate phenotypes, the social determinants of complexity, and complexity itself. Therefore, a change in the heritability of complexity could be driven by a change in the relative importance of genes on intermediating characteristics. In family demography, Udry (1996) argued more specifically that the genetic influence on voluntary behavioral outcomes, e.g. entering parenthood and marriage, will increase in societies with low levels of social constraints. Genetic predispositions have more room to express themselves in contexts where variation in individual behavior is high and is less restricted by formal and informal norms. Indeed, a number of studies using twin data show that genes are more important for fertility motivation (Rodgers et al 2001) and fertility (Kohler et al. 1999; 2002; Tropf et al. 2015a) for cohorts that began their transition to adulthood after then onset of the SDT. Therefore, I expect *the heritability of family trajectory complexity and its components will increase across birth cohorts in the United States* (H2), especially for those cohorts characterized by the SDT.

Data & Methods

Sample & Sequence Definition

The HRS[27] is a biannual prospective panel with information on family formation, which recently collected molecular genetic data from their respondents. The original HRS cohort was first sampled in 1992 and consisted of men and women born between 1931-1941, ages 51-61. A second study cohort of men and women born before 1924, the Asset and Health Dynamics among the Oldest Old, was collected the following year. The two study cohorts were collected simultaneously in 1998 when the third and fourth cohorts were introduced, the Children of the Great Depression born between 1924-1930 and the War Babies born between 1942-1947. Since then a refreshment sample has been added every three waves, i.e. six years.

I estimate the heritability of family sequence complexity and selected components of complexity: the age at first birth, number of children ever born, the age at first marriage, number of marriages, and the number of divorces.[28] An overview of these variables is displayed in Table 1. Retrospective and prospective information on childbearing as well as union formation and dissolution are used to reconstruct individuals' family life courses as sequences from age 18 to 45. Marital histories can be completely reconstructed using retrospective data for the first four marriages. Therefore, complexity is not calculated for individuals who report more than four marriages. Unfortunately, marital histories were collected differently for the second cohort, which makes it difficult to identify the start and end dates of more than one marital union. Therefore, I also omit the Asset and Health Dynamics among the Oldest Old HRS cohort from the complexity analyses. Sequences consist of 18 consecutive states, which can be never married (S), married (M), or widowed or divorced (D). All states can be further differentiated between having no children or having one or more children (e.g. MNC or MC). Note that the results presented below are robust to more differentiated sequence alphabets, e.g. for higher parity births and higher order marriages. Cohabitation and residential histories have not been extensively collected by the HRS and therefore cannot be included in the sequence alphabet.

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[27] The HRS (Health and Retirement Study) is sponsored by the National Institute on Aging (grant number NIA U01AG009740) and is conducted by the University of Michigan. 1992-2014 RAND Fat Files, Cross-Wave: Polygenic Score Data, RAND HRS Longitudinal File 2014, and the RAND HRS Family Data 2014 public use datasets. Produced and distributed by the University of Michigan with funding from the National Institute on Aging (grant number NIA U01AG009740). Ann Arbor, MI, 2018. For more information, visit: http://hrsonline.isr.umich.edu/.

[28] Individuals that did not have children, that did not marry, or those who married but did not divorce are included in the analyses with zeros for the number of children ever born, the number of marriages, and the number of divorces variables, respectively.

Estimating Genetic Similarity

Saliva samples were collected during enhanced face-to-face interviews during the 2006, 2008, 2010, and 2012 waves for 15,708 respondents. Genotyped data measuring a sample of approximately 2.4 million single nucleotide polymorphisms (SNP) was obtained from respondents' saliva samples using the Ilumina HumanOmni2.5 BeadChips.[29] SNPs are DNA nucleotide pairs that vary within a population. For example, at a single position in the genome some individuals may have the nucleotide cytosine, while others have thymine. The variants of each SNP are called alleles and the alleles that are the second most common in a population are termed minor alleles. Using the SNPs, genetic similarity is estimated as:

$$A_{jk} = \frac{1}{N}\sum_i \frac{(x_{ij}-2p_i)(x_{ik}-2p_i)}{2p_i(1-p_i)}, \tag{1}$$

where N is the number of genetic markers, and x_{ij} and x_{ik} are the number of minor alleles at SNP i for individuals j and k, and p is the minor allele frequency. The matrix A containing the genetic similarity estimates between all respondent pairs is called the genetic relationship matrix (GRM). I calculate the GRMs using all autosomal[30] SNPs with a minor allele frequency above one percent in the sample to ensure that genetic similarity is based on variants that are relatively common within a population.[31] I then prune the sample for cryptic relatedness ($A_{ij} \geq 0.025$), i.e. persons genetically comparable with second-degree cousins. It has been shown that genetically similar individuals also share similar environments, which could bias my heritability estimates by including variation attributable to shared environments. Although it has been demonstrated that the violation of this assumption does not substantially bias GREML estimates (Conley et al. 2014), I nonetheless follow convention and prune the data for cryptic relatedness.

Estimating Heritability

I use GCTA-GREML to estimate the heritability of family life course complexity and its components (see Domingue et al. 2016 for an introduction on applications with social demographic traits; see also Yang et al. 2011). The underlying assumption of GREML is that

[29] For detailed information on the collection and preparation on the genotypic data, see the Quality Control Report for Genotypic Data at http://hrsonline.isr.umich.edu/sitedocs/genetics/HRS2_qc_report_SEPT2013.pdf prepared by the University of Washington.

[30] Autosomal chromosomes are non-sex chromosome pairs 1-22.

[31] GREML assume that the average effect size on the outcome of interest per standardized SNP is minute and normally distributed. The distribution assumption also assumes that SNPs with low minor allele frequencies have larger effects. Therefore, rare alleles are removed to ensure heritability estimates are not based on a rare variant found only in a select population (Yang et al. 2017, pp.1307–1308).

if phenotypic variation is attributable to genetic variants, then individuals who are more similar genetically should be more similar phenotypically. GREML utilizes random effects modeling to quantify the proportion of trait variance that is attributable to genomic differences. Formally, a given phenotype, y, is modeled as:

$$y = X\beta + g + \epsilon, \tag{2}$$

where Xβ is a matrix of covariates and their coefficients, g is a vector of random effects and ϵ a vector of errors. As the name GREML indicates, the model is estimated using restricted maximum likelihood. It is a common sensitivity test to include several principle components extracted from the GRM as covariates to adjust for population stratification, i.e. differences in minor allele frequencies that are attributable to ancestral differences.[32] However, this adjustment has been criticized as it may correct for differences that are meaningful for the trait being studied and can lead to underestimated heritability estimates. Nonetheless, I estimate additional models using four ancestral principle components (see Table A1 in the manuscript appendix). The GRM enters the model through the variance component of the random effects:

$$g \sim Normal(0, \sigma_g^2 A). \tag{2a}$$

This means that the individual random effects are normally distributed with a mean of zero and a variance of σ_g^2, which denotes the additive genetic variance captured by the SNPs. The GRM, A, builds the variance-covariance structure of the random effect. Note that standard assumptions apply for GREML models, e.g. that ϵ is independent of X and g, and normally distributed. Heritability, h^2, is then defined as the proportion of total variance attributable to the variance of the random effects. Formally,

$$Var(y) = Var(g) + Var(\epsilon) = \sigma_g^2 + \sigma_\epsilon^2, \tag{2b}$$

where the variance of y, Var(y), is equal to the variance component of the random effect, σ_g^2, plus the residual variance, σ_ϵ^2. Subsequently, heritability is estimated as the variance component of the random effect, σ_g^2, divided by the total variance of y, $\sigma_g^2 + \sigma_\epsilon^2$:

$$h^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_\epsilon^2}. \tag{2c}$$

[32] This is commonly called the "chopsticks problem", which arises when subgroups have different allele frequencies that coincide with a phenotype that is culturally rather than biologically determined (Hamer & Sirota 2000). For example, persons of Asian and European ancestry will systematically differ on SNP variants that would coincide with the different probability of chopstick use between the two subgroups.

This modeling approach belongs to the class of mixed linear modeling, similar to the cross-classified random effects approach used in chapter 2. Heritability is essentially an intraclass correlation coefficient commonly used in sociological research. However, rather than estimating country and cohort random effects to decompose the complexity variance attributable to differences across countries and cohorts, the random effect above is used to decompose the variance into a genetic and an environmental component.

I estimate SNP heritabilities for a pooled HRS sample as well as heritabilities for 20-year birth cohorts. Due to the issue of population stratification, I follow the convention in the literature and restrict my sample to self-identified Non-Black and Non-Hispanics. I include all respondents with valid[33] information in the GREML analyses for sequence complexity, age at 1st birth, number of children, age at 1st marriage, number of marriages and number of divorces. Therefore, my analysis sample size varies between heritability estimates. The analysis samples consist of between 7,975 and 11,891 Non-Black and Non-Hispanics men and women born between 1915 and 1964 before removing cryptically related individuals. I use the GCTA[34] program package to conduct all analyses (see Yang et al. 2011).

Results

Trends in Sequence Complexity & its Components

Summary statistics for the Non-Black Non-Hispanic HRS sample connected with genetic data are displayed in Table 1. Averages by year of birth for family sequence complexity are displayed in Figure 1.[35] As can be seen in Table 1, average family sequence complexity is 0.21 for men and 0.18 for women. The upper-left panel of Figure 1 shows that average complexity has increased for both men and women across birth cohorts from 1915 to 1960. However, complexity increased more drastically within a shorter timeframe for women: average complexity was approximately 0.17 for women born in 1940, but increased to 0.2 for women born in 1950.

[33] I exclude implausible information from the analyses, i.e. values below the 1st percentile or above the 99th percentile. A possible explanation for the prevalence of implausible answers may lie in the fact that the HRS was not originally conceived as a life history study. Simultaneous consistency checks that are now common were either not implemented or not available at the time. However, results including these values do differ substantially or chance the substantive conclusions.
[34] http://cnsgenomics.com/software/gcta/#Overview
[35] Please note that these are summary statistics for the sample upon which heritabilities will be estimated and are not weighted to correct for differential sampling probabilities. They nonetheless give an accurate picture of the demographic history of US cohorts born in the early to mid-20th century.

Table 1: Summary Statistics for Family Sequence Complexity and its Components

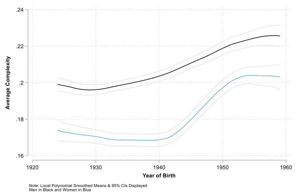
	Complexity	Age at 1st Birth	Number of Children	Age at 1st Marriage	Number of Marriages	Number of Divorces
Men	0.21	26.34	2.97	24.42	1.42	0.49
	(0.06)	(5.46)	(1.69)	(5.33)	(0.80)	(0.77)
Women	0.18	23.70	2.86	22.30	1.42	0.48
	(0.08)	(4.88)	(1.66)	(5.93)	(0.78)	(0.77)
Total	0.19	24.81	2.91	23.22	1.42	0.48
	(0.08)	(5.30)	(1.67)	(5.78)	(0.79)	(0.77)
N	9,429	10,618	11,189	9,903	11,891	11,547

Note: Data not weighted

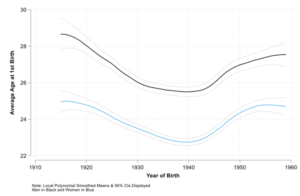
Men tend to have their first child and marry later than women at age 26 and 24, respectively, as presented in Table 1. The trend in the average age of these two transitions follows a U-shaped pattern. For example, women born in 1920 entered marriage around age 26, which dropped to nearly 21 for women born 10 years later, only to rise to age 24 for women born in 1960. On average, men and women had nearly the same number of children, marriages, and divorces: approximately 2.9 children, 1.4 marriages, and 0.4 divorces. Men and women also experienced similar trends for the number of children born and number of divorces. Individuals born in 1915 had on average 2.8 children, which increased to 3.3 for the 1930 cohort before decreasing to 2.4 for the 1950 cohort. The number of divorced increased nearly linearly between the 1915 and 1950 birth cohorts from nearly 0 to just over 0.6. The trend in the number of marriages is slightly different for men and women. Both increase in from 1.3 to nearly 1.5 between the 1915 and 1940 birth cohort, but the number of marriages decreases to nearly 1.3 for men born in 1960 while remaining constant for women. This could be related to an increase in cohabitation among men (Koops et al. 2017, p.544).

Figure 1: Average Family Sequence Complexity and its Components by Year of Birth

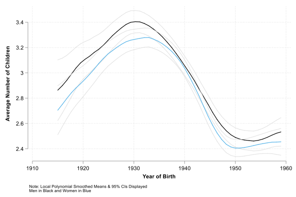
Sequence Complexity



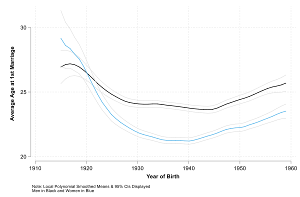
Age at 1st Birth



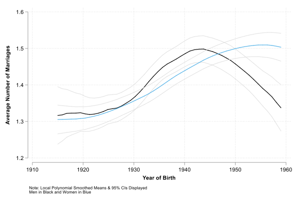
Number of Children



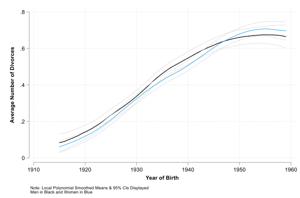
Age at 1st Marriage



Number of Marriages



Number of Divorces



GREML Heritability Estimates

The unadjusted SNP heritability estimates from GREML analyses on the pooled sample are displayed in Table 2 along with their standard errors, p-values, and sample sizes. Cohort-specific unadjusted SNP heritability estimates are presented in Figure 2, which are estimated using 20-year cohorts to ensure a sufficiently large sample (N ≈ 5,000 for $h^2 \approx 0.2$) (see Visscher et al. 2014). For example, the 1925 heritability estimate is based on men and women born between 1915 and 1935. Confidence intervals estimated with maximum likelihood have been shown to be upwards biased (see Schweiger et al. 2016), making it difficult to discern which estimates are statistically different from zero. I therefore mark heritability estimates that are statistically different from zero ($p \leq 0.05$) in blue. SNP heritability estimates adjusted for four principle components provided by the HRS data providers to account for population stratification are displayed in Table A1 in the manuscript appendix.

Table 2: SNP Heritability Estimates for Family Sequence Complexity and its Components from GREML on Pooled Samples

	Complexity	Age at 1st Birth	Number of Children	Age at 1st Marriage	Number of Marriages	Number of Divorces
h^2	0.107	0.263	0.169	0.274	0.262	0.209
SE	0.049	0.045	0.044	0.047	0.040	0.041
p-Value	0.006	0.000	0.000	0.000	0.000	0.000
N	7,975	8,933	9,432	8,398	10,058	9,766

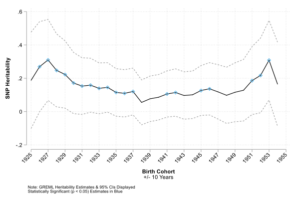
Note: Heritabilities, standard errors, p-values, and sample sizes from GREML analyses displayed

As can be seen in Table 2, family sequence complexity is heritable. Roughly 11 % of the total variation in complexity can be attributed to common genetic variants. The estimates of the single family demographic components are heritable to a greater degree. For the age at first birth, genes account for about 26 % of the total variation, and for the number of children genes account for about 17 %. Interestingly, heritability estimates for the age at first marriage, number of marriages, and number of divorces are similar or even higher than the fertility estimates. Over 27 % and 26 % of variation in the age at 1st marriage and the number of marriages, respectively, can be accounted for by common genetic variants. The number of divorces is nearly 21 % heritable. These estimates may be small compared to the heritability of anthropomorphic traits, e.g. up to 56 % for height and 43 % for BMI (Conley et al. 2014; Yang et al. 2015), but are larger than the heritability of some sociological and psychological traits, e.g. up 19 % for socioeconomic status and 21 % for certain personality traits (Marioni et al. 2014; Trzaskowski et al. 2014; Power & Pluess 2015).

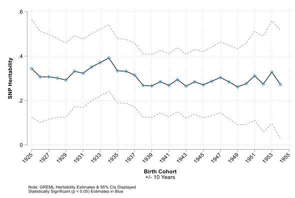
I do not find evidence for birth cohort differences for the heritability for complexity due to the large standard errors of my heritability estimates. I will nonetheless shortly discuss the trends I observe. First the heritability estimates for family sequence complexity follows a U-shaped pattern: The estimated complexity heritabilities of the 1917-1937 and the 1943-1963 cohorts are the largest, approximately 30 %, while many of the estimated heritabilities between 1928-1948 and 1938-1958 cohorts are not statistically different from zero at conventional levels. A similar U-shaped trend, albeit not statistically significant, can be observed for the number of divorces. The number of divorces for the 1918-1938 and 1944-1964 cohorts is roughly 40 % and 45 % heritable, respectively, while the heritability estimate is less than 20 % for the 1933-1953 cohort.

Figure 2: SNP Heritability Estimates from GREML on 20-Year Birth Cohorts

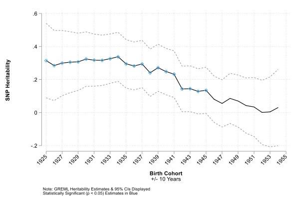
Sequence Complexity



Age at 1st Birth



Number of Children



Age at 1st Marriage

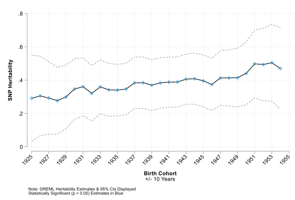
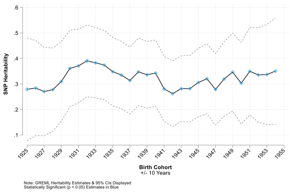
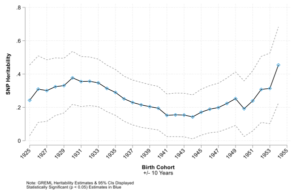


Figure 2 continued

Number of Marriages



Number of Divorces



While my heritability estimates for the number of children declines nearly linearly across birth cohorts, the estimates for the age at first marriage increases. Estimated heritability for the number of children decreases from over 30 % for the 1915-1935 cohort to 0 for the 1943-1963 cohort. This is the only difference that is statistically significant at conventional levels. Between the 1915-1935 and 1943-1963 cohorts, the heritability of the age at first marriage increased from about 30 % to 50 %. I find no apparent trends for the heritability of the age at first birth and the number of marriages across birth cohorts.

Discussion

In this chapter, I applied for the first time a biodemographic approach to the study of family life course complexity using methods developed in molecular genetics. Specifically, I estimated the heritability of family life course complexity as well as the age of first birth, number of children, age of first marriage, number of marriages, and number of divorces using GCTA-GREML on HRS data. Based on findings from behavioral genetics research on twins, I hypothesized that family life course complexity as well as its components will be heritable (H1). Further, based on arguments by Udry (1996; see also Kohler et al. 2006) that heritability increases in contexts characterized by fewer social constraints, I hypothesized that the heritability of family life course complexity and its components will increase across birth cohorts in the United States (H2). While I do indeed find moderate heritabilities for complexity as well as other family demographic indicators (H1), I find little systematic evidence for increasing heritability (H2).

My results support micro-biosocial models that family demographic (e.g. Kohler et al. 2006; Udry 1996) and sociological (Freese 2008) outcomes are heritable. On account of the composite nature of family life course complexity – incorporating both fertility, union formation, and union dissolution – it seems plausible that genetic factors influence complexity directly through biological mechanisms and indirectly through intermediate phenotypes, such as personality. My SNP heritability estimates for fertility are slightly higher than those estimated by Tropf and colleagues (2015b) on a pooled sample of UK and Dutch women. As would be expected, my SNP heritabilities for marriage and divorce are somewhat lower than earlier estimates using twin data (Johnson et al. 2004 for marriage; Jocklin et al. 1996; McGue & Lykken 1992 for divorce). In sum, my analyses corroborate previous literature that family demographic behavior is heritable and demonstrate that even composite life course outcomes are influenced by genes.

However, my results do not systematically validate Udry's (1996) hypothesis that the genetic influence on voluntary behavioral outcomes, e.g. entering parenthood and marriage, will increase in societies characterized by the SDT. A possible explanation might lie in an additional hypothesis made by Udry (1996, p.328) that has received less attention: "The more similar the social constraints faced by individuals in a society (…) the higher the proportion of variance in their behavior that is controlled by biological differences in the population". While shifts in value orientations and legal opportunities for divorce may be similar between the US and many northwestern European countries, the universality of those constraints may be higher in generous European welfare states that are secularized to a higher degree. Further analyses, given adequate sample sizes, should estimate heritabilities separately by educational group or socioeconomic status.

There are limitations to the estimation of heritability with GREML and using SNPs (see Krishna Kumar et al. 2016 for an overview). The GCTA-GREML approach is only valid for traits with genetic variants located throughout the entire genome that are weakly associated with that trait (Domingue et al. 2016). This is because the GRM only approximates genome-wide genetic similarity if the sample of SNPs and their association with a trait are a reasonably good proxy for the entire genome. The SNP heritability estimate may be biased if a genetic variant with an exceptionally large association is missing. However, it is unlikely that my heritability estimate for sequence complexity, which is per definition highly polygenic due to its composite nature, is biased in such a manner.

A further limitation that GCTA shares with other estimation methods for heritability, is the "black box" nature of heritability. Without knowing the loci associated with complexity and the phenotypic effects of those loci, it is not possible to follow the causal biological and social pathways connecting genetic factors with complexity. Future research could use bivariate GREML models to test the genetic correlation between two phenotypes, such as complexity and personality (Deary et al. 2012; Lee et al. 2012). This would allow scholars to inch towards untangling the causal mechanisms involved in the heritability of family life course complexity.

What role can social policy play in societies where social demographic outcomes are heritable? This question has been debated since Murry & Herrnstein's (1994) deeply controversial book "The Bell Curve" argued that the United States had become a "genotocracy": a society where social stratification is based on genetic differences and social policy only could alleviate the consequences of those differences. Recently, Conley & Fletcher (2017) published a systematic critique of the perspective that stratification patterns in western societies are genetically based and unalterable. Even if heritability is extremely high, it does not indicate genetic determinism as the impact of genetic factors on social outcomes is dependent on social environments and must be contextualized. Although I do not find evidence for cross-temporal change in heritability, a comparison of my estimates with findings using European data (e.g. Tropf et al. 2015b) indicates strong gene-environment interactions (see also Tropf et al. 2016). The reaction of individuals with similar genotypes will vary across social contexts, especially when institutions affect the relationship between intermediate phenotypes and social processes. My results in no way support arguments that stratification patterns are static due to genetic influences and cannot be altered by social policy.

My results demonstrate that holistic life course outcomes are heritable and that life course sociologists should begin to incorporate biodemography into their research. A first starting point is to estimate heritabilities for more life course outcomes that are of interest. For example, the heritability of life course patterns derived from cluster analysis and the heritability of deviations from those patterns. Depending on the outcomes of those analyses, life course sociologists should incorporate existing educational and fertility polygenic risk scores into their analyses that estimate the associations between individual characteristics and life course patterns. This could give sociologists leverage on whether educational attainment is causally associated with the choice to follow a certain life course path or whether unobserved intermediate phenotypes, e.g. cognitive ability, are confounding our analyses.

Acknowledgements The analyses presented below were concluded at Princeton University under supervision of Dalton Conley.

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Appendix

Table A1: Adjusted SNP Heritability Estimates for Family Sequence Complexity and its Components from GREML on Pooled Sample

	Complexity	Age at 1st Birth	Number of Children	Age at 1st Marriage	Number of Marriages	Number of Divorces
h^2	0.078	0.176	0.167	0.196	0.181	0.140
SE	0.052	0.050	0.047	0.052	0.045	0.046
p-Value	0.053	0.000	0.000	0.000	0.000	0.000
N	7,540	8,437	8,599	7,944	9,489	9,216

Note: Heritabilities, standard errors, p-values, and sample sizes from GREML analyses displayed; Adjusted for 10 ancestral principle components

CHAPTER 6

CONCLUSION

The overarching aim of my dissertation was to systematically study the complexity of family life courses in Europe and the United States during the 20th century. Until now, there has been little descriptive research on how family life course complexity varies across socio-historic contexts (see Elzinga & Liefbroer 2007 for an exception). Moreover, no studies have attempted to estimate associations between individual and societal characteristics, and family life course complexity. Rather than conceptualizing complexity in terms of the occurrence of single events and transitions, I added a temporal and processual dimension that emphasizes the unpredictability of individual life courses. It is important for scholars and policy makers alike to better understand complexity, because it is likely related to the production and reproduction of social inequalities (e.g., McLanahan & Percheski 2008), the effectiveness of traditional welfare policies (e.g., Dannefer 2003; Morel et al. 2012), and population development (e.g., Schmidt et al. 2012). To conclude, I first review the findings and contributions of each chapter. Then I discuss the limitations of how life course complexity was conceptualized and operationalized in my studies. Finally, I present an integrated framework to guide further research on the complexity of family trajectories.

Contributions to the Literature

I developed and empirically tested hypotheses from the three core theoretical perspectives – cultural, economic, and institutional – as well as an emerging biodemographic perspective on family life course complexity throughout four chapters. These theoretical perspectives were originally developed for the analysis of single life course states or transitions (see White 1994 for parental home leaving; Smock 2000 for cohabitation; Amato & James 2010 for divorce; Balbo et al. 2013; and Morgan & Taylor 2006 for fertility). However, I applied theses theoretical perspectives to the complexity of holistic life course trajectories rather than a series of life course states or transitions. Table 1 displays a summary of the hypotheses from each chapter, the theoretical perspective from which they were derived, and to what extent they were supported by the empirical findings.

Table 1: Overview of Chapter Hypotheses, Theoretical Perspectives, and Empirical Support

Hypotheses	SDT	Economic Uncertainty	Institutional Arrangements	Bio-Demography	Empirical Support
Chapter 2: Time & Space					
1) Complexity has increased across cohorts.	**X**				~
2) Complexity is highest in social democratic countries, then conservative countries, and lowest in southern and eastern European countries.			**X**		+
3) Complexity variation across cohorts is country-specific.			**X**		~
4) Complexity varies more across countries than cohorts.			**X**		+
Chapter 3: Family Policies					
1) Familizatizon is associated with less complexity.			**X**		+
2) Defamilization is associated with more complexity.			**X**		+
3) Liberalization is associated with more complexity.			**X**		+
4) Policies during early adulthood matter most.			**X**		~
Chapter 4: Parental Resources					
1.1) Parental resources are associated with more complexity.	**X**				−
1.2) This association has weakened across birth cohorts.	**X**				−
2.1) Parental resources are associated with less complexity.		**X**			+
2.2) This association has strengthened across birth cohorts.		**X**			+
Chapter 5: Genetic Factors					
1) Complexity is moderately heritable.				**X**	+
2) Heritability will increase across cohorts.				**X**	−

Note: In the final column, + denotes empirical support, ~ denotes partial empirical support, and – denotes no empirical support.

The second chapter of this dissertation sought to provide a clear description of family life course complexity across European countries in the 20th century. My descriptive findings had important implications for mainstream sociological and demographic theories on family life course complexity (see Besbris & Khan 2017 on the importance of description for theory). I started with the observation that the literature lacked a clear and systematic description of how life course complexity varied across countries and cohorts. The comparative literature, had up to then, compared family trajectories either across birth cohorts within a single country (Baizan et al. 2002; Bras et al. 2010; Chaloupková 2010; Robette 2010) or between a small set of countries (Potarca et al. 2013). No research had attempted to directly compare change in family formation over historical time with cross-national differences, although this is important for two reasons. First, putting cross-temporal differences in direct perspective with cross-national differences can serve as a benchmark to assess the extent of change over time. Second, this type of comparison simultaneously appraises two prominent research traditions: the ideational account of the Second Demographic Transition (SDT) and the institutional arguments of comparative life course sociology.

Therefore, I sought to assess (1) how family life courses vary across birth cohorts, (2) how family life courses vary across countries, and (3) whether family life courses vary more across birth cohorts or across countries. I formulated four hypotheses (see Table 1): First, I formulated the hypothesis that family trajectories have become more differentiated across birth cohorts, based on the expectations of the SDT thesis (Van de Kaa 1987; 2001; Lesthaeghe 1995; 2010). Second, based on institutional accounts in the differential life course literature that commonly use welfare state typologies (Esping-Andersen 1990; 1999; Mayer 1997; 2004), I stated that family trajectories are most differentiated in social democratic countries, followed by conservative countries, and least differentiated in southern European countries as well as in eastern European countries. My third and fourth hypotheses were based on the idea that welfare state institutions can imped the effects of postmaterialism on family demographic behavior. Specifically, that family trajectory variation across birth cohorts is country-specific and that family trajectory differentiation varies more across countries than across birth cohorts. Indeed, my analyses using retrospective data from SHARELIFE with cross-classified random effects modeling supported all my hypotheses, albeit to varying degrees.

I do find a trend towards increasing complexity across all European countries, which supports that traditional narrative of the SDT. Economic growth, educational expansion, and welfare state development enabled shift toward postmaterialism among cohorts born in the mid-20th century. This ideational shift led to delayed marriage and parenthood as well as more cohabitation, childlessness, and divorce. However, the cross-national differences I find far surpass change over time, even in Sweden where complexity increased the most. I argue that the dissemination of postmaterialism over time can be inhibited by national institutional arrangements that lag this cultural change. This not only accounts for the country-specific complexity trends I find, but also why change over time is so minor. The results of this second chapter clearly indicate the importance of institutional differences across countries, although persisting cultural differences may also play an important role (e.g. Hajnal 1965; Reher 2005).

My third chapter took a closer look at institutional differences across European countries and family life course complexity. However, rather than relying on broad welfare state regime types, I examined the role of specific policy dimensions. Specifically, 1) what are the associations between familizing, defamilizing, and liberalizing family policies and family life course complexity and 2) does the timing of family policies within the life course moderate those associations? Based on common theoretical approaches in the comparative welfare state and life course sociological literature (Esping-Andersen 1990; 1999; Mayer 2004; 2009), I formulated four hypotheses (see Table 1): First, familizing policies, which actively or implicitly incentivize early marriage and parenthood (Saraceno 2016), are associated with less complex family life courses. Second, defamilizing policies, which decrease the opportunity costs involved with divorce and nonmarital childbirth (Lohmann & Zagel 2016; Daly 2011), are associated with more complex family life courses. Third, policies that liberalize divorce and abortion legislation are associated with more complex family life. Finally, I hypothesized that early policy experiences will have the largest associations, because early impulses can have path dependent and cumulative effects.

Indeed, my results support the idea that cross-national differences, at least in part, are driven by differences in national family policy arrangements. First and foremost, I find that familization decreases the complexity of family life courses for both men and women, especially during early and prime adulthood. Defamilization and liberalization are associated with family complexity to a lesser degree and are dependent on life course timing: Liberalization during early adulthood increase men’s complexity, while defamilization in early adulthood increase women’s complexity. Conversely, liberalization during early adulthood increase women’s complexity, while defamilization in early adulthood increase men’s complexity. However, the variation of life course complexity that is attributable to cross-national differences and the amount of variation that family policies can account for is quite small. The vast majority, over 75 %, of complexity variation can be traced to individual differences.

The next step of my dissertation was to look at the relationship between individual characteristics and family life course complexity. I concentrated on parental resources and socio-economic background for two reasons: First, two of the prominent theories on complexity – the SDT thesis and the economic uncertainty framework – posit contrasting relationships between parental resources and family life course complexity (see Lesthaeghe & Johan Surkyn 1988; Furstenberg 2008; Mills & Blossfeld 2013). Second, socioeconomic background is an individual characteristic that precedes young adults' transition to adulthood and family formation. Therefore, in chapter 4, I formulated two sets of competing hypotheses relating to the research questions (see Table 1): 1) what is the association between parental resources and early family life course complexity and 2) has the association between parental resources and complexity changed across birth cohorts. According to the SDT, young adults from socioeconomically advantaged backgrounds should be the forerunners of the SDT, but eventually more complex family life courses should be a universal phenomenon. Hence, high parental resources should be associated with more complex family formation trajectories, but this should weaken over time. However, if economic uncertainty is linked to more complex life courses, then low parental resources should be associated with increasingly higher levels of complexity.

The empirical results of chapter 4 clearly support the economic uncertainty framework and puts pressure, like chapter 2, on the SDT thesis. In this chapter I used US data, specifically the NLSY79 and NLSY97, rather than European data, because the effects of globalization and economic uncertainty are likely greater in liberal welfare states. Although parental resources are negatively associated with the complexity of family life courses for the 1981-1984 cohort, there are no substantively or statistically significant associations for the 1961-1964 cohort. My findings particularly highlight the importance of another perspective: McLanahan's (2004) diverging destinies framework. While parental education has substantial effects on complexity for white men, the effects of childhood family structure for white women and African Americans are far more substantial. Further, even after adjusting for individuals' educational attainment, the strength of the childhood family structure effect is still far from negligible. Further research on the association between socioeconomic background, parental resources, and life course complexity needs to incorporate family structure, not just empirically but also theoretically.

My final chapter sought to delve deeper into individual factors that may affect the complexity of individual family life courses: the genome (Conley 2016; D'Onofrio & Lahey 2010; Freese

2008). When one considers the components of family life course complexity, for example the age at first birth and completed fertility (e.g. Mills & Tropf 2015), it is likely that genetic factors may influence the complexity of family lives. Not only do genetic factors directly influence fertility through biological pathways, but indirectly by means of conscious and subconscious decision-making (Kohler et al. 2006). Further, intermediate phenotypes partially determined by genetic factors likely precede, moderate, or confound the relationships between social determinants and the different facets of family life course complexity (Freese 2008). In addition, it has been argued that genetic factors will become more important in societies with low levels of social constraints on family demographic behavior (Udry 1996; Kohler et al. 2006). Therefore, I tested whether complexity as well as its components are heritable and whether heritability had increased across birth cohorts.

Using GCTA-GREML on retrospective life history and molecular genetic data in the HRS for the first time (Yang et al. 2011; Yang et al. 2010), I found that family life course complexity and its components are indeed heritable. The consideration of genes can enhance our current understanding of complexity in two respects: First, incorporating genetic influences in the analysis of complexity can increase predictive power. Indeed, the influence of genetic factors on complexity is similar to the amount of variation attributed to cross-national differences in chapter 2. Second, considering genetic and biological pathways aids in estimating the impact of intermediating variables net of genetic confounding.

While I do not find evidence that the heritability of complexity varied across birth cohorts, I maintain that biodemographers have concentrated too heavily on Udry's (1996, p.328) hypothesis on the level of social constraints. It is also important that social constraints be universal and not socially stratified. The relationship between the stratification of social constraints and heritability may have received less attention, because most research on cross-temporal heritability is on Nordic countries (Rodgers et al. 2001; Kohler et al. 1999; 2002; 2004). As I demonstrated in chapter 4, social constraints on family demographic behavior are likely not uniform across social classes in the United States. Increasing social and economic constraints on family demographic behavior could even lead to decreasing heritability (see also Tropf et al. 2015). My recommendation for family sociologists, demographers, and life course scholars is that biodemographic approaches should be systematically incorporated into our research, both theoretically and methodologically.

Where do we stand when it comes to family life course complexity? When reviewing Table 1, it is clear that evidence for the SDT theory is scarce: complexity has only moderately increased across European birth cohorts compared to cross-national differences (chapter 1, H1 & H2) and the relationship between socioeconomic background and complexity was negative and increasing across US cohorts (chapter 4 H1.1 & H1.2), rather than positive and decreasing. The strengthening negative relationship indeed supports the economic uncertainty framework, there are however two aspects that warrant further thought. First, my results indicate that family structure is more relevant than parental education or income. Although family structure in the United States is certainly related to economic uncertainty, other mechanisms that are less related with globalization and deindustrialization are also possible, e.g. socialization, social control, and stress. Second, the country-specific cohort trends in Europe, i.e. earlier increases in Sweden, Denmark, and Switzerland (chapter 2, H3), do not correspond with the globalization framework. However, it is an empirical question whether younger European cohorts more closely resemble the US cohorts I studied or not.

As it currently stands, *the SDT as a theory has little empirical validity*. The increase in complexity, even in the United States, is relatively small and cross-national variation seems to be much more important. Rather than ideational change, *increasing economic uncertainty, changing childhood family structure, and differences in national institutional arrangements are the most important factors for differences in complexity between and within socio-historic contexts*. Increasingly precarious economic circumstances during young adulthood and an increasing reliance on parents during the transition to adulthood seems to have fostered higher levels of complexity. Further, changing institutional arrangements may not only account for increasing complexity within European countries, especially in Sweden and Denmark, but especially for cross-national differences in Europe. Specifically, a shift from familistic to defamilistic family policy additionally spurred by the liberalization of divorce and abortion legislation. Finally, *genetic factors matter for the complexity of individuals' family life courses* and could likely contribute to the predictive power of my models, especially from chapter 4. Future research should continue to incorporate other theoretical perspectives that I was unable to include. Especially promising are compositional arguments based on local marriage and partner markets (e.g. Esping-Andersen & Billari 2015 on gender norms).

The Quantitative and Qualitative Limitations of Complexity

The studies in this dissertation have numerous limitations, which have mostly been discussed in the individual chapters. Some of these have pertained to the violation of model assumptions, issues with retrospective life history data, and incomplete information. However, the studies I have presented have used the full potential of the available data to answer my research questions. In this section, I will discuss a limitation that is common among all studies: the conceptualization and operationalization of complexity. The limitations of complexity can be divided into two components: quantitative and qualitative. While the quantitative limitations relate to the measurement of complexity, the qualitative limitations reflect the meaning of complexity for individuals. The latter is especially important to understand the effects of increasing inequality for society as a whole.

The complexity index is both extremely nuanced and versatile, but simultaneously ambiguous and variable. The distribution of the complexity index is highly dependent on the number of sequence states. A highly differentiated sequence alphabet will lead to a positively skewed distribution, while a very simple sequence alphabet can lead to a bimodal distribution with zero as the first mode. Generally, the modal value will reflect the complexity of the most common sequence, for example a pathway of two children within marriage. If the state space is small, often because residential and cohabitation histories are missing, then zeros will become increasingly common, e.g. single without children, even though these persons may have very complex lives. If the state space is large, which often results by including birth parity within each union type (e.g. M1C to M12C), then persons with more than three children will have extremely high values. As with any other dependent variable, the distribution can have serious implications on the model fit. Therefore, it is important to run a large number of sensitivity analyses with different sequence alphabets to ensure that results aren't being driving by meaningless differences in state definitions. This may become even more relevant as large families becomes increasingly rare, while serial cohabitation and marriage become more common.

Another issue with the complexity index lies in the interchangeability of complexity values. Two individuals that have the same number of transitions into distinct states with the same durations will have identical complexity values, even if the states are different. The sequences in Figure 1 demonstrate the issue of having qualitatively distinct family life courses with equal complexity values. Each example sequence consists of 5 distinct states with two consecutive time points, e.g. years, within each state, the first being in the parental home (P). The first sequence could be a very common sequence in 20th century Europe where the parental home is followed by two years in marriage (M) followed by two years married with one, two, and finally three children (M1C, M2C, M3C, respectively). The second and third sequences are similar, but the second sequence replaces marriage with cohabitation (C, C1C, C2C, C3C) and the third sequence cohabitation with singlehood (S, S1C, S2C, S3C). The fourth sequence is similar to the third, but being single with a second and third child is replaced with having a child within the parental home (P1C) and cohabiting with a child (C1C), respectively. The last sequence consists of the parental home, marriage, divorce, followed by marriage and divorced with a child (P, M, D, M1C, D1C).

Although these five sequences are the same quantitatively, most would not say they are similarly complex. This is the quantitative side of the qualitative limitation of complexity. Which of these sequences is the least complex? Intuitively, some may say the first sequence is the least complex, because it is still relatively common in most European societies and the United States and therefore relatively predictable. And which sequence is the most complex? Sequences four and five experience multiple changes in union and residential status, which may mean more unpredictability. For many, having a second or third child within the same union does not make life courses increasingly complex, but rather having a second and third child within a new union. There are two possibilities to account for this: adjust the sequence alphabet, e.g. do not differentiate between children within the same union, or weight complexity by state duration. These two strategies were adapted throughout my analyses and were discussed where necessary.

Figure 1: Qualitatively Distinct Sequences of Equal Complexity

Sequence 1	P	P	M	M	M1C	M1C	M2C	M2C	M3C	M3C
Sequence 2	P	P	C	C	C1C	C1C	C2C	C2C	C3C	C3C
Sequence 3	P	P	S	S	S1C	S1C	S2C	S2C	S3C	S3C
Sequence 4	P	P	S	S	S1C	S1C	P1C	P1C	C1C	C1C
Sequence 5	P	P	M	M	D	D	M1C	M1C	D1C	D1C
	t_1	t_2	t_3	t_4	t_5	t_6	t_7	t_8	t_9	t_{10}

Sequence analysis is a method to quantitatively measure and analyze qualitative states across the life course. However, the normative evaluation of complexity as a sequence based metric is challenging. Complexity as a process outcome results from numerous decisions and events taken throughout the life course (Abbott 2005), each of which are associated with subjective meanings that may vary across individuals. A strategy to evaluate subjective meanings of complexity could lie in different normative narratives. For example, complexity generated by personal decisions to form and dissolve informal and formal unions is good from a perspective of individual freedom from institutional constraints. Traditional religious narratives will likely judge increasing complexity based on union dissolution negatively, while increasing complexity based on higher fertility would be seen more positively. Complexity generated by precarious states, such as single parenthood, would be assessed negatively from an economic perspective. Weighting sequence complexity by individual durations in certain states, as was done in chapter 2 and by Van Winkle and Fasang (2017), could shed light on how complexity may be evaluated from individualistic, religious, and economic narratives. The best possibility to empirically identify individuals' normative evaluations would be the use of prospective data, such as the NLSY79 and NLSY97 in chapter 4, to match subjective data with complexity.

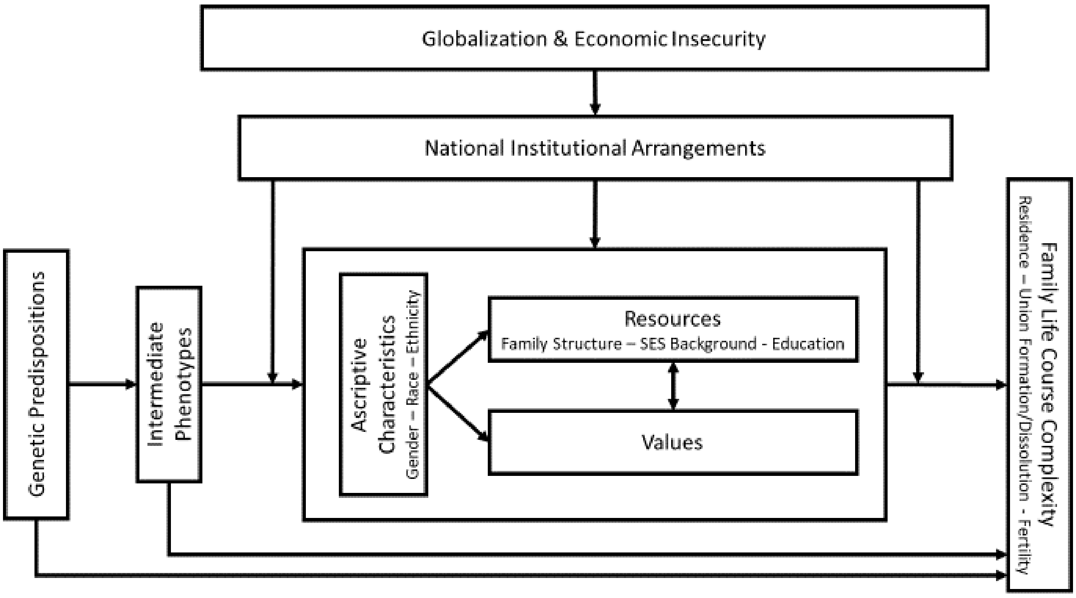
Comparing theoretical perspectives, especially the SDT and globalization accounts, allow me to gain some leverage on what increasing complexity may mean for individuals and society. The SDT thesis and the economic uncertainty framework have different perspectives on the social meaning and consequences of increasing complexity (see Zimmermann & Konietzka 2017 for a discussion on destandardization). The SDT as a theory takes an optimistic stance on the complexity of family lives and commonly assumes that increasing differentiation is associated with less institutional control over life courses and more individual freedom when making family formation decisions (Beck 2009; 1994). The economic uncertainty framework tends to take a more pessimistic stance and associate increasing social inequality as well as increasing life course risks and instability with complexity (McCall & Percheski 2010; McLanahan & Percheski 2008). As discussed above, I find little evidence for the SDT thesis in its current state, but rather show an increasingly strong relationship between socioeconomic background and the complexity of family life courses. Even if more complex family formation is the result of increasing freedom of choice, the options open to disadvantaged young adults are likely more constrained when compared to their counterparts from more advantaged backgrounds.

A Framework for Future Research

It is important to continue to study the causes of family life course complexity if future research is to understand its consequences for individuals and societies. The chapters in this dissertation, for the most part, looked at each theoretical perspective individually or compared them with the

SDT thesis. Future research should follow an integrated framework to understand the evolution of individual and societal levels of family life course complexity in a holistic manner. To conclude this work on family life course complexity, I would like to introduce such a framework. Figure 1 displays how external economic factors, national institutions, genetic predispositions, and individual resources and values interact to determine levels of family life course complexity.

Figure 1: An Integrated Framework for Family Life Course Complexity



At the micro-level, in the center of Figure 2, individual resources, values, and ascriptive characteristics have a direct effect on family life course complexity. As I have shown with relatively young US birth cohorts, higher parental resources and educational attainment will lead to less complex family trajectories. For more these cohorts, this relates to delayed marriage and parenthood as well as more stable marriages. However, resources and values will in part be predetermined by genetic predispositions through intermediate traits, for example cognitive ability and personality traits that affect educational attainment. Genetic predispositions will also affect family life course complexity directly through biological mechanisms, although to a lesser degree.

At the top of the framework lies globalization and economic uncertainty as well as national institutional arrangements. The impact of external economic factors will be first be filtered through national education, labor market, family, and welfare state institutions before affecting the micro-level mechanisms that determine the complexity of individual family life courses (Mills & Blossfeld 2003; 2005; 2013). There are then three pathways through which external economic factors and institutions can mutually effect complexity. First, macro-level factors can impact how genetic predispositions and intermediate phenotypes effect individual resources and values (Udry 1996; Kohler et al. 2006). Second, economic and institutional factors can affect individual values, access to education, and the distribution of resources. Finally, these higher-level factors can moderate the relationship between individual characteristics and complexity, for example via the moderation of individual decision-making processes (see Gauthier 2007 for fertility).

As my studies were conducted across European welfare states and the United States, I can extrapolate some information on how these three policy pathways may work. First, compared with other results with European data (e.g. Tropf et al. 2015), it is likely that the influence of genetic factors on family complexity will only increase if welfare institutions ensure that economic and social constraints on behavior are universally low across all social strata. However, this hypothesis that egalitarian welfare regimes facilitate higher heritabilities needs to be rigorously tested. Second, as was demonstrated in chapter 2, policy arrangements can influence the composition of populations, which in turn is associated with complexity, e.g. educational expansion may induce a population level decrease in complexity. As demonstrated by the third pathway and chapter 3, policies may influence decision-making processes related to complexity: policies that facilitate a work-family balance and gender-egalitarian division of labor will increase family life course complexity, while policies that strengthen familial obligations will reduce it. Until the consequences of family life course complexity are better understood, I refrain from making policy recommendations.

Future research on family life course complexity will need to be ambitious, both theoretically and methodologically, to grasp current developments that I was unable to study. In the coming years, European panel data will be linked with molecular genetic data that will enable researchers to account for all the factors in Figure 1 simultaneously. However, research needs to be conducted on the consequences not just the causes of family life course complexity. Are less complex family lives good for individuals socioeconomic standing, for their health, and for their wellbeing? Or will less complex family lives signal fewer familial ties and greater loneliness in older age? Under which conditions is complexity associated with advantageous or disadvantageous outcomes? Are other family states needed for other areas of the world, for example living with extended relatives rather than in the parental home? Research on the complexity of life courses is and will continue to be an exciting and fruitful area for generations to come.

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SUMMARY

Many scholars have claimed that patterns of family formation and living arrangements have undergone great changes in European societies during the twentieth century. No research has attempted to directly compare change in family formation over historical time with cross-national differences. The aim of my first empirical chapter (chapter 2) is not only to investigate (1) how family life courses vary across birth cohorts, and (2) how family life courses vary across countries, but (3) whether family life courses vary more across birth cohorts or across countries. This study uses SHARELIFE data from 14 European countries and a new methodological approach, combining complexity metrics developed in sequence analysis with cross-classified multilevel modeling, is used to simultaneously quantify the proportions of variance attributable to birth cohort and country differences.

In my second empirical chapter (chapter 3), I address two research questions: 1) what is the association between family policies and family life course complexity and 2) does the timing of family policies within the life course moderate this association? I combine numerous data sources to estimate the relationships between three family policy dimensions and the complexity of family life courses. Information on family allowances, maternity leave, parental leave, and paternity leave, etc., from 1924-2008 are used to generate familization, defamilization, and liberalization policy indexes. Retrospective data from the third wave of the Survey of Health, Ageing and Retirement in Europe (SHARELIFE) are used to reconstruct the family life courses of individuals from age 15-50, born 1924-1956, from 15 European countries. Finally, I estimate the associations between my policy indexes and sequence complexity in country and time fixed effects regression models.

In my third empirical chapter (chapter 4), I investigate whether the differentiation of family life courses is attributable to the pathways of young adults from advantaged or disadvantaged backgrounds. Specifically, I address two research questions: 1) what is the association between parental resources and the early family life course complexity and 2) has the association between parental resources and complexity changed across birth cohorts. Data from the 1979 and 1997 National Longitudinal Survey of Youth (NLSY79 and NLSY97) show that complexity is higher among disadvantaged young adults. In my last empirical chapter (chapter 5), I address that fact that life course sociologists have neglected the potential role of genetic factors when studying life course complexity. I apply retrospective life history and molecular genetic data from the US Health and Retirement Study to a genome-wide complex trait analysis (GCTA) to study the heritability of life course complexity. Gene-environment interactions are incorporated by estimating heritably by birth cohort.

I conclude that the SDT as a theory has little empirical validity. The increase in complexity, even in the United States, is relatively small and cross-national variation seems to be much more important. Rather than ideational change, increasing economic uncertainty and differences in national institutional arrangements are the most important factors for cross-national and cross-cohort differences in complexity. A shift from familistic to defamilistic family policy and the liberalization of divorce spurred the differentiation of family life courses. Finally, genetic factors matter for the complexity of individuals' family life courses and could likely contribute to the predictive power of future statistical models.

ZUSAMMENFASSUNG

In den Sozialwissenschaften gibt es eine weitverbreitete Auffassung, dass sich die Familiengründung und Lebensformen in europäischen Gesellschaften während des 20. Jahrhunderts verändert haben. Bisher wurden Veränderungen in Familienverläufen über die Zeit nicht direkt mit länderspezifischen Unterschieden verglichen. Ziel des ersten empirischen Kapitels (Kapitel 2) war es zu untersuchen wie Familienverläufe 1) über Geburtskohorten hinweg variieren, 2) über Länder hinweg variieren, und 3) ob Familienverläufe mehr über die Zeit oder über Länder hinweg variieren. Auf Basis von SHARELIFE Daten für 14 europäische Länder wird eine innovative methodische Herangehensweise entwickelt, indem Komplexitätsmaße aus der Sequenzanalyse mit der Mehrebenenmodellierung zusammengeführt werden.

Das zweite empirische Kapitel (Kapitel 3) stellt zwei Forschungsfragen: 1) was ist der Zusammenhang zwischen Familienpolitik und der Komplexität von Familienverläufen und 2) wird dieser Zusammenhang durch den Zeitpunkt im Lebensverlauf moderiert, in dem die jeweilige Familienpolitik gilt? Um den Zusammenhang zwischen Familisierungs-, Defamilisierungs-, und Liberalisierungsindezes und der Komplexität von Familienverläufen zu schätzen werden Informationen über u.a. Elterngeld, Bildung, Renten, und Scheidungs- und Abtreibungsgesetze von 1924-2008 herangezogen. Anhand der SHARE Daten für 15 Länder werden die Zusammenhänge zwischen den Familienpolitikindizes und der Komplexität der Familienverläufe in Regressionsmodellen mit Länder und Kohorten Fixed-Effects geschätzen.

Im nächsten Kapitel untersuche ich, ob die Differenzierung von Familienverläufen eher auf die Verläufe von jungen Erwachsenen aus sozial benachteiligten oder besser gestellten Herkunftsfamilien zurückzuführen sind. Ich stelle zwei Forschungsfragen: 1) was ist der Zusammenhang zwischen elterlichen Ressourcen und der Komplexität von Familienverläufen im jungen Erwachsenenalter; und 2) hat der Zusammenhang zwischen elterlichen Ressourcen und der Komplexität von Familienverläufen sich über Geburtskohorten hinweg verändert? Daten des 1979 und 1997 US National Longitudinal Survey of Youth (NLSY79 und NLSY97) zeigen, dass Komplexität eher bei jungen Erwachsenen aus benachteiligten Elternhäusern angestiegen ist. Das abschliessende empirische Kapitel verwendet retrospektive Lebensverlaufs- und molekular genetische Daten der US Health und Retirement Study (HRS) in einer genome-wide complex trait analysis (GCTA) an, um die Vererbbarkeit von Lebensverlaufskomplexität in Familienverläufen zu untersuchen. Gene-Umwelt Interaktionen werden hinzugenommen, indem Vererbbarkeit nach Geburtskohorten geschätzt wird.

Ich komme zu dem Schluss, dass die Theorie des Zweiten Demografischen Übergangs wenig empirische Validität hat. Die Zunahme von Komplexität, auch in den USA, ist relativ klein und Länderunterschiede sind viel bedeutsamer. Nicht kulturelle normative Veränderungen, sondern zunehmende ökonomische Unsicherheit und sozialpolitische Institutionen scheinen die wichtigsten Faktoren für kohorten- und länderspezifischen Unterschiede in der Komplexität von Familienverläufen zu sein. Eine Umstellung von einer familisierenden auf eine defamilisierende Familienpolitik zusammen mit der Liberalisierung von Scheidungsgesetzen führt zu einem Anstieg der Differenzierung von Familienverläufen. Abschließend lässt sich festhalten, dass genetische Faktoren die Komplexität von individuellen Familienverläufen ebenfalls beeinflussen und ihre Berücksichtigung die Vorhersagekraft von statistischen Modellen in Zukunft erhöhen könnte.